

09/830,338  
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## Neurobiology: NAIP

NAIP (for neuronal apoptosis inhibitory protein) is a protein that inhibits apoptosis of neurons and its gene is often mutated in severe cases of spinal muscular atrophy, a disease characterized by motor neuron degeneration. NAIP is expressed in mouse macrophages, in anterior horn and motor cortex neurons of normal brains, in human fetal neurons and in adult choroid plexus cells. NAIP expression is increased after phagocytic events and during infection with *L. pneumophila*. There are at least three NAIP gene copies that encode full-length mRNA, NAIP1, 2, and 3.

### Closest Matches:

Click on the **Product Name** to find out more information or to shop for a product.

Product	Cat.#	Isotype	Epitope	Applications	Species
<a href="#">NAIP2 (A-17)</a>	sc-11068	goat IgG	internal (m)	WB, IHC	m, r
<a href="#">NAIP2 (T-17)</a>	sc-11069	goat IgG	internal (m)	WB, IHC	m, r
<a href="#">NAIP1 (S-20)</a>	sc-11067	goat IgG	N-terminus (m)	WB, IHC	m, r, h
<a href="#">NAIP1 (E-20)</a>	sc-11066	goat IgG	N-terminus (m)	WB, IHC	m, r
<a href="#">NAIP (P-19)</a>	sc-11064	goat IgG	C-terminus (h)	WB, IHC	m, r, h
<a href="#">NAIP (L-18)</a>	sc-11062	goat IgG	N-terminus (m)	WB, IHC	m, r
<a href="#">NAIP (P-16)</a>	sc-11059	goat IgG	N-terminus (h)	WB, IHC	m, r, h
<a href="#">NAIP (G-20)</a>	sc-11060	goat IgG	C-terminus (h)	WB, IHC	h

### Additional NAIP and related products:

Product	Cat.#	Isotype	Epitope	Applications	Species
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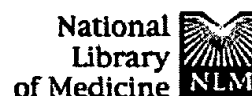


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- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.

Search	Most Recent Queries	Time	Result
#8 Related Articles for PubMed (Select 9302277)		16:44:44	<u>198</u>
#6 Related Articles for PubMed (Select 12547647)		16:39:35	<u>424</u>
#4 Search #3 AND antibody		16:36:06	<u>1</u>
#3 Related Articles for PubMed (Select 7813013)		16:35:34	<u>142</u>

Clear History

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Dec 11 2003 12:53:39

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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:50 ; Search time 24 Seconds

(without alignments)  
2473.422 Million cell updates/sec

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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	946	67.4	1232 4 US-09-493-784-2	Sequence 2, Appl1
3	939	66.9	1151 3 US-08-836-134-23	Sequence 23, Appl1
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6	56	4.0	56 4 US-08-657-759-22	Sequence 22, Appl1
7	54	3.8	54 4 US-08-657-759-21	Sequence 21, Appl1
8	50	3.6	50 3 US-08-975-080-26	Sequence 26, Appl1
9	47	3.3	47 3 US-08-975-080-13	Sequence 13, Appl1
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11	18	1.3	18 4 US-08-657-759-23	Sequence 23, Appl1
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13	8	0.6	64 4 US-09-205-258-580	Sequence 580, Appl
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RESULT 3
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; Sequence 23, Application US/08836134A
; Patent No. 6020127
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneljuk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Ikeda, John
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6020127
; FILE REFERENCE: Mutations Causative of Spinal Muscular Atrophy
; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-836-134-23

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
US-09-493-784-23
Sequence 23, Application US/09493784
Patent No. 6429011
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
APPLICANT: Mahadevan, Mani S.
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Ikeda, John
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6429011
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCES: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/09/493,784
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 08/836,134
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 1151
TYPE: PRT
ORGANISM: Homo sapiens
US-09-493-784-23
Query Match 66.3%; Score 939; DB 4; Length 1151;

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATOQKASDERISQDPHNLLPELSALLGLDAVALAKELEEBEOKERAKKQKNSQMRSE 60
D 10 MATOQKASDERISQDPHNLLPELSALLGLDAVALAKELEEBEOKERAKKQKNSQMRSE 69
QY 61 AKRLKFTVYEPYSSWIPOBMAAGFFFTGVNSGICQFCCSLILFGAGLTRLPIDHKRP 120
D 70 AKRLKFTVYEPYSSWIPOBMAAGFFFTGVNSGICQFCCSLILFGAGLTRLPIDHKRP 129
QY 121 HPDCCFLNKDYNIAKVDIIVKNLSRLRGGMRRQSEBARLASFRNPFYVQGISPCV 180
D 130 HPDCCFLNKDYNIAKVDIIVKNLSRLRGGMRRQSEBARLASFRNPFYVQGISPCV 189
QY 181 LSEAGFVFTGKQDVTQCFSCGCGCLGMBEGDDPMKEHAKMPKCEFLRKSSEETIYI 240
D 190 LSEAGFVFTGKQDVTQCFSCGCGCLGMBEGDDPMKEHAKMPKCEFLRKSSEETIYI 249
QY 241 QSYKGFVDITGHEFNANSMQRELPMAASAYCNDISIFAYEBELRDSFKDMRESAVYALA 300
D 250 QSYKGFVDITGHEFNANSMQRELPMAASAYCNDISIFAYEBELRDSFKDMRESAVYALA 309
QY 301 KAGLFYTGIKDIYQCFSCGCGCLGMBEGDDPLDDHTRCFPNCPLOMKSABVTPLDS 360
D 310 KAGLFYTGIKDIYQCFSCGCGCLGMBEGDDPLDDHTRCFPNCPLOMKSABVTPLDS 369
QY 361 RGELELLETTSESNLEDSIAVGPIVPENAQBAQFOBAKUNLEOLRAAYTSASFRHS 420
D 370 RGELELLETTSESNLEDSIAVGPIVPENAQBAQFOBAKUNLEOLRAAYTSASFRHS 429
QY 421 LDDISDLATDHLGCDLSIAKHSKIPQEBLVLPYEVGNLNSVWCVEGEGSGKTVLL 480
D 430 LDDISDLATDHLGCDLSIAKHSKIPQEBLVLPYEVGNLNSVWCVEGEGSGKTVLL 489
QY 481 KKIAPFMAAGCCPLNRFQLVFVLSSTRPREGLASIIDOLLEKESVTMCKRNIIO 540
D 490 KKIAPFMAAGCCPLNRFQLVFVLSSTRPREGLASIIDOLLEKESVTMCKRNIIO 549
QY 541 QLNQVFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVTRNARDIRRYLETILEIK 600
D 550 QLNQVFLDDYKEICSIPOVIGKLIQKNHLSRTCLLIIVTRNARDIRRYLETILEIQ 609
QY 601 AEPYNTVCIIRKLFSHNMTRLRKFMVYFGKQOSLOKIQTPLFVAACAHMFOYPPDS 660
D 610 AEPYNTVCIIRKLFSHNMTRLRKFMVYFGKQOSLOKIQTPLFVAACAHMFOYPPDS 669
QY 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELALGFSCCFEENDDLAAGVDED 720
D 670 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELALGFSCCFEENDDLAAGVDED 729
QY 721 EDLTMCLMSKFTAOQLRPFYRFLSPAFQEFAGRLIELDSDROEHODLGLYHLKOINS 780
D 730 EDLTMCLMSKFTAOQLRPFYRFLSPAFQEFAGRLIELDSDROEHODLGLYHLKOINS 789
QY 781 PMMTVSAVNNFLANYVSSLPSTKAGPKIVSHLHLVDNKESLENISENDYILKIQPEISIQ 840
D 790 PMMTVSAVNNFLANYVSSLPSTKAGPKIVSHLHLVDNKESLENISENDYILKIQPEISIQ 849
QY 841 MOLLRLGIMQICPOAYFSMWSEHLLVTLAKTAYQSNVTAACSPVLOQLQRTLTGALNL 900
D 850 MOLLRLGIMQICPOAYFSMWSEHLLVTLAKTAYQSNVTAACSPVLOQLQRTLTGALNL 909
QY 901 QYFDPHPSLSLRSIHFPRIKGNKTSPPRAHFSVLETCFDSQVPTIDODYASAFEPNEM 960
D 910 QYFDPHPSLSLRSIHFPRIKGNKTSPPRAHFSVLETCFDSQVPTIDODYASAFEPNEM 969
QY 961 ERNLAEKEDNVKSYMDQORRASPDLSTGYWKLSPKQYKIPCLEVDVNDIDVVGOMLEIL 1020
D 970 ERNLAEKEDNVKSYMDQORRASPDLSTGYWKLSPKQYKIPCLEVDVNDIDVVGOMLEIL 1029
QY 1021 MTFVSAQRIEILHNHSGFIESIRPALELSKASVTMCSISKLELSAEBELLTLTPSLE 1080

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Db 1030 MTVFSASQRIELHNSRGFIESIRPALBLSKASVTKCSISKLELSAEOELLTLPSLE 1089  
 QY 1081 SLEVSGTISODQIPNLDKFLCKELSYDLGNINVSIVIPPEPNFHMEXLIIQISA 1140  
 Db 1090 SLEVSGTISODQIPNLDKFLCKELSYDLGNINVSIVIPPEPNFHMEXLIIQISA 1149  
 QY 1141 E 1141  
 Db 1150 E 1150

RESULT 5  
 US-08-657-759-22  
 ; Sequence 22, Application US/08657759  
 ; Patent No. 6511828

GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.

TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS

TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSES: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,759

FILING DATE: 31-MAY-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 75 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-657-759-22

Query Match 5.3%; Score 75; DB 4; Length 75;

Best Local Similarity 100.0%; Pred. No. 2.6e-64;

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 QEBEARLASRMPFYVQGISPCVLSBAGVFTGKQDTVCGCGGCLGWMEGDDPMKX 216

Db 1 QEBEARLASRMPFYVQGISPCVLSBAGVFTGKQDTVCGCGGCLGWMEGDDPMKX 60

QY 217 HAKFPKCEFLRSKX 231

Db 61 HAKFPKCEFLRSKX 75

RESULT 6

US-08-657-759-24

; Sequence 24, Application US/08657759

; Patent No. 6511828

; GENERAL INFORMATION:

; APPLICANT: Thompson, Craig B.

; APPLICANT: Duckett, Colin S.

; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS

;; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)  
 ;; NUMBER OF SEQUENCES: 58  
 ;; CORRESPONDENCE ADDRESS:  
 ;; ADDRESSES: Arnold, White & Durkee  
 ;; STREET: P.O. Box 4433  
 ;; CITY: Houston  
 ;; STATE: Texas  
 ;; COUNTRY: United States of America  
 ;; ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,759

FILING DATE: 31-MAY-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 56 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-657-759-24

Query Match 4.0%; Score 56; DB 4; Length 56;

Best Local Similarity 100.0%; Pred. No. 4.1e-46;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 VGVAAALAKAGLFYTGKIDIVQCFSCGCLKXQEGDDPLDDHTRCPPNCPFLONNK 349

Db 1 VGVAAALAKAGLFYTGKIDIVQCFSCGCLKXQEGDDPLDDHTRCPPNCPFLONNK 56

RESULT 7

US-08-657-759-21

; Sequence 21, Application US/08657759

; Patent No. 6511828

; GENERAL INFORMATION:

; APPLICANT: Thompson, Craig B.

; APPLICANT: Duckett, Colin S.

; TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS

; TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,759

FILING DATE: 31-MAY-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 56 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-657-759-21

TELEPHONE: (512) 418-3000  
 TELEFAX: (512) 474-7577  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 54 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-657-759-21

Query Match 3.8%; Score 54; DB 4; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-44;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

78 POEAAAGFYTGKSGIGCCSLIFGAGLRLPIEDHKRPHPCGFIAND 131  
 1 POEAAAGFYTGKSGIGCCSLIFGAGLRLPIEDHKRPHPCGFIAND 54

## RESULT 8

US-08-975-080-26  
 Sequence 26, Application US/08975080  
 Patent No. 6245523  
 GENERAL INFORMATION:  
 APPLICANT: Altieri, Dario C.  
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
 TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
 STREET: 1800 M Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036-5869  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/975,080  
 FILING DATE: 20-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/031,435  
 FILING DATE: 20-NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Adler, Reid G.  
 REGISTRATION NUMBER: 30,988  
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-467-7000  
 TELEFAX: 202-467-7176  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-975-080-26

Query Match 3.6%; Score 50; DB 3; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-40;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

306 YTGKIDIVQCFSCGCGCKEKQEGDDPLDHTRCFPCNCPFIONKSSAETV 355  
 1 YTGKIDIVQCFSCGCGCKEKQEGDDPLDHTRCFPCNCPFIONKSSAETV 50

## RESULT 9

US-08-975-080-13

Sequence 13, Application US/08975080  
 Patent No. 6245523  
 GENERAL INFORMATION:  
 APPLICANT: Altieri, Dario C.  
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
 TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
 STREET: 1800 M Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036-5869  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/975,080  
 FILING DATE: 20-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/031,435  
 FILING DATE: 20-NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Adler, Reid G.  
 REGISTRATION NUMBER: 30,988  
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-467-7000  
 TELEFAX: 202-467-7176  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 47 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-975-080-13

Query Match 3.3%; Score 47; DB 3; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-37;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

159 EEARLASFRNMPFYVGISPCVLSAGVFYTGKQDVTQCFSCGCLG 205  
 1 EEARLASFRNMPFYVGISPCVLSAGVFYTGKQDVTQCFSCGCLG 47

US-08-657-759-20  
 Sequence 20, Application US/08657759  
 Patent No. 6511828  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Craig B.  
 TITLE OF INVENTION: Duckett, Colin S.  
 TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,759  
FILING DATE: 31-MAY-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARCD:220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-657-759-20

Query Match 1.4%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8,2e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 RSEAKRLKTFVYEPYSSWI 77  
DB 1 RSEAKRLKTFVYEPYSSWI 20

RESULT 11  
US-08-657-759-23  
Sequence 23, Application US/08657759  
Patent No. 6511828  
GENERAL INFORMATION:  
APPLICANT: Thompson, Craig B.  
TITLE OF INVENTION: HUMAN AND DROSOPHILA INHIBITORS  
NUMBER OF SEQUENCES: 58  
TITLE OF INVENTION: OF APOPTOSIS PROTEINS (IAPs)  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,759  
FILING DATE: 31-MAY-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARCD:220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-657-759-23

Query Match 1.3%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6,3e-10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 AYEELRLDSFKDWPRESA 293

DB 1 AYEELRLDSFKDWPRESA 18

RESULT 12  
US-09-252-991A-28407  
Sequence 28407, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rudenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.116  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 28407  
LENGTH: 870  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28407

Query Match 0.6%; Score 9; DB 4; Length 870;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 AGSGKTIVLL 480  
DB 55 AGSGKTIVLL 63

RESULT 13  
US-09-205-258-580  
Sequence 580, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 580
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-580

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Query Match      0.64; Score 8; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      39 EEEEXKER 46
      |||||
Db      29 EEEEXKER 36

RESULT 14
US-08-511-485-16
Sequence 16, Application US/08511485
Patent No. 5919912

```

```

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
NUMBER OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-Aug-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-16

```

```

Query Match      0.64; Score 8; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      193 DTVQCFSC 200
      |||||
Db      34 DTVQCFSC 41

RESULT 15
US-09-201-936-16
Sequence 16, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liaton, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0

```



SEQ ID NO 16  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-16

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 68;  
Pred. No. 9.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTWQCSFC 200  
DB 34 DTWQCSFC 41

RESULT 16  
US-09-252-991A-24674  
Sequence 24674, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 24674  
LENGTH: 183  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24674

Query Match  
Best Local Similarity 100.0%; Score 8; DB 4; Length 183;  
Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 LSLSTRP 511  
DB 154 LSLSTRP 161

RESULT 17  
US-08-301-162-18  
Sequence 18, Application US/08301162  
Patent No. 6022546  
GENERAL INFORMATION:  
APPLICANT: Knapp, Stefan  
APPLICANT: Ziegelmaler, Robert  
APPLICANT: Kupper, Hans  
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The  
PREPARATION THEREOF AND THE USE THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/301,162  
FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/167,128  
FILING DATE: 07/623,086  
APPLICATION NUMBER: US 07/623,086  
FILING DATE: 06-DEC-1990  
APPLICATION NUMBER: DE P3940598.2  
FILING DATE: 08-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Fleisher, Raz E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 02481.1005-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 428 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-301-162-18

Query Match  
Best Local Similarity 100.0%; Score 8; DB 3; Length 428;  
Pred. No. 47;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
DB 395 FGAGLTRL 402

RESULT 18  
US-09-461-240-18  
Sequence 18, Application US/09461240  
Patent No. 6326008  
GENERAL INFORMATION:  
APPLICANT: Knapp, Stefan  
APPLICANT: Ziegelmaler, Robert  
APPLICANT: Kupper, Hans  
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The  
PREPARATION THEREOF AND THE USE THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/461,240  
FILING DATE: 16-DEC-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/301,162  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/167,128  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/623,086  
FILING DATE: 06-DEC-1990  
APPLICATION NUMBER: DE P3940598.2  
FILING DATE: 08-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Fleisher, Raz E.  
REGISTRATION NUMBER: 34,331  
REFERENCE/DOCKET NUMBER: 02481.1005-00000

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-461-240-18

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 428;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 105 FGAGLTRL 112

395 FGAGLTRL 402

RESULT 19

US-09-968-927-18

Sequence 18, Application US/09968927

Patent No. 6419925

GENERAL INFORMATION:

APPLICANT: Knapp, Stefan

Ziegelmaier, Robert

Kupper, Hans

TITLE OF INVENTION: Toxoplasma Gondii Antigens, The

Preparation Thereof and the Use Thereof

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &amp;

Dunne

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,927

FILING DATE: 03-Oct-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/301,162

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US/08/167,128

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 07/623,086

FILING DATE: 06-DEC-1990

APPLICATION NUMBER: DE P3940598.2

FILING DATE: 08-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: Fleisher, Raz E.

REGISTRATION NUMBER: 34,331

REFERENCE/DOCKET NUMBER: 02481.1005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 428 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-968-927-18

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 428;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 105 FGAGLTRL 112

395 FGAGLTRL 402

RESULT 20

US-09-198-452A-170

Sequence 170, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffls, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

thereof and uses thereof, in particular for the diagnosis, prevention

and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 170

LENGTH: 441

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-170

Query Match

Best Local Similarity 100.0%; Score 8; DB 4; Length 441;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 102 LILFGAGL 109

135 LILFGAGL 142

RESULT 21

US-08-511-485-10

Sequence 10, Application US/08511485

Patent No. 5919912

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish &amp; Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/511,485

FILING DATE: 04-AUG-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 07540/002001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 496 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: both  
MOLECULE TYPE: protein  
US-08-511-485-10

Query Match 0.6%; Score 8; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOCFSC 200  
DB 59 DTVOCFSC 66

RESULT 22  
US-09-212-971-10  
Sequence 10, Application US/09212971B  
Patent No. 6107041  
GENERAL INFORMATION:  
APPLICANT: Korneljuk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009002  
CURRENT APPLICATION NUMBER: US/09/212,971B  
CURRENT FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: 60/017,354  
EARLIER FILING DATE: 1996-04-26  
EARLIER APPLICATION NUMBER: 60/030,590  
EARLIER FILING DATE: 1996-11-14  
EARLIER APPLICATION NUMBER: 08/800,929  
EARLIER FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-212-971-10

Query Match 0.6%; Score 8; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOCFSC 200  
DB 59 DTVOCFSC 66

RESULT 23  
US-08-800-929A-10  
Sequence 10, Application US/08800929A  
Patent No. 6133437  
GENERAL INFORMATION:  
APPLICANT: Korneljuk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF  
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: DISEASE  
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Ribing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996

APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bleker-Brady, Kristina

REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045

TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-929A-10

Query Match 0.6%; Score 8; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOCFSC 200  
DB 59 DTVOCFSC 66

RESULT 24  
US-09-617-053A-10  
Sequence 10, Application US/09617053A  
Patent No. 6300492  
GENERAL INFORMATION:  
APPLICANT: Korneljuk, Robert G  
APPLICANT: Mackenzie, Alexander E  
APPLICANT: Liston, Peter  
APPLICANT: Baird, Stephen  
APPLICANT: Tsang, Benjamin K  
APPLICANT: Pratt, Christine  
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
FILE REFERENCE: 07891/009003  
CURRENT APPLICATION NUMBER: US/09/617,053A  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/800,929  
PRIOR FILING DATE: 1997-02-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-617-053A-10

Query Match 0.6% Score 8; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOQCSC 200  
DB 59 DTVOQCSC 66

## RESULT 25

US-09-201-936-10  
Sequence 10, Application US/09201936  
Patent No. 6541457  
GENERAL INFORMATION:  
APPLICANT: Kormeluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
EARLIER FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-10

Query Match 0.6% Score 8; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVOQCSC 200  
DB 59 DTVOQCSC 66

## RESULT 26

US-09-205-258-573  
Sequence 573, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 573  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: SITE  
LOCATION: (409)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-205-258-573

Query Match 0.6%; Score 8; DB 4; Length 567;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEOOER 46  
Db 483 EEEEOOER 490

RESULT 27  
US-09-303-064-55  
Sequence 55, Application US/09303064  
Patent No. 6221619  
GENERAL INFORMATION:  
APPLICANT: MAINE, Gregory T.  
APPLICANT: HUNT, Jeffery C.  
APPLICANT: BROJANAC, Susan  
APPLICANT: JYH-TSING SHEU, Michael  
APPLICANT: CHOVAN, Linda E.  
APPLICANT: TYNER, Joan D.  
APPLICANT: HOWARD, Lawrence V.  
APPLICANT: PARMELEY, Stephen F.  
APPLICANT: REMINGTON, Jack S.  
APPLICANT: ARAUJO, Fausto  
APPLICANT: SUZUKI, Yashuhiro  
APPLICANT: LI, Shuli  
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF  
FILE REFERENCE: 6361 US P1  
CURRENT APPLICATION NUMBER: US/09/303,064  
CURRENT FILING DATE: 1999-04-30  
EARLIER APPLICATION NUMBER: 09/086,503  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 667  
TYPE: PRT  
ORGANISM: Toxoplasma gondii  
US-09-303-064-55

Query Match 0.6%; Score 8; DB 3; Length 667;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
Db 542 FGAGLTRL 549

RESULT 28  
US-09-086-503-55  
Sequence 55, Application US/09086503A  
Patent No. 6329157  
GENERAL INFORMATION:  
APPLICANT: MAINE, Gregory T.  
APPLICANT: HUNT, Jeffery C.  
APPLICANT: BROJANAC, Susan  
APPLICANT: JYH-TSING SHEU, Michael  
APPLICANT: CHOVAN, Linda E.  
APPLICANT: TYNER, Joan D.  
APPLICANT: HOWARD, Lawrence V.  
TITLE OF INVENTION: ANTIGEN COCKTAILS AND USES THEREOF  
FILE REFERENCE: 6361 US 01  
CURRENT APPLICATION NUMBER: US/09/086,503A  
CURRENT FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 55

LENGTH: 667  
TYPE: PRT  
ORGANISM: Toxoplasma gondii  
US-09-086-503-55

Query Match 0.6%; Score 8; DB 4; Length 667;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
Db 542 FGAGLTRL 549

RESULT 29  
US-08-434-730-14  
Sequence 14, Application US/08434730  
Patent No. 5637463  
GENERAL INFORMATION:  
APPLICANT: Dalton, Stephen  
APPLICANT: Kochan, Jarema P  
APPLICANT: Osborne, Mark A  
TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN  
INTERACTIONS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: USA  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,730  
FILING DATE: 04-May-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Semionow, Raina  
REGISTRATION NUMBER: 39022  
REFERENCE/DOCKET NUMBER: 9069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201)235-4391  
TELEFAX: (201)235-2363  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 968 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-434-730-14

Query Match 0.6%; Score 8; DB 1; Length 968;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082  
Db 229 TLPSLESL 236

RESULT 30  
US-08-560-005-2  
Sequence 2, Application US/08560005  
Patent No. 6001354  
GENERAL INFORMATION:  
APPLICANT: Pot, David A.  
APPLICANT: Williams, Lewis T.

APPLICANT: Jefferson, Anne Bennett  
APPLICANT: Majerus, Philip W.  
TITLE OF INVENTION: No. 6001354e1 Grb2 Associating Protein and Nucleic  
NUMBER OF INVENTION: Acids Encoding Therefor  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560.005  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-0624000  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 976 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-560-005-2

Query Match  
Best Local Similarity 0.6%; Score 8; DB 3; Length 976;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1075 TLPSLESL 1082  
Db 14 TLPSLESL 21

RESULT 31  
US-09-195-868-14  
Sequence 14, Application US/09195868  
Patent No. 6090621  
GENERAL INFORMATION:  
APPLICANT: KAVANUGH MD, MICHAEL  
APPLICANT: POT PH.D., DAVID  
APPLICANT: WILLIAMS M.D., LEWIS T.  
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE  
NUMBER OF INVENTION: 5-PHOSPHATASES (Sips)  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/195,868  
FILING DATE:  
CLASSIFICATION:  
APPLICATION NUMBER: US/09/195,868

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FIRESTONE, LEIGH H.  
REGISTRATION NUMBER: 36,831  
REFERENCE/DOCKET NUMBER: 1182.004  
TELEPHONE: 510-923-2707  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 976 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-195-868-14

Query Match  
Best Local Similarity 0.6%; Score 8; DB 3; Length 976;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1075 TLPSLESL 1082  
Db 14 TLPSLESL 21

RESULT 32  
US-09-418-540-2  
Sequence 2, Application US/09418540  
Patent No. 6296848  
GENERAL INFORMATION:  
APPLICANT: POT, David A.  
APPLICANT: WILLIAMS, Lewis T.  
APPLICANT: Majerus, Anne Bennett  
TITLE OF INVENTION: No. 6296848e1 Grb2 Associating Protein and Nucleic  
NUMBER OF INVENTION: Acids Encoding Therefor  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/418,540  
FILING DATE: 14-OCT-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/560.005  
FILING DATE: 17-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 2307K-0624000  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 976 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-418-540-2

Query Match  
0.6%; Score 8; DB 3; Length 976;

Best Local Similarity 100.0%; Pred. No. 99;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1075 TLPSLESL 1082  
14 TLPSLESL 21  
Db

RESULT 33  
US-09-969-528-2  
; Sequence 2, Application US/09969528  
; Patent No. 6472197  
; GENERAL INFORMATION:  
; APPLICANT: Pot, David A.  
; Williams, Lewis T.  
; Jefferson, Anne Bennett  
; Majerus, Philip W.  
; TITLE OF INVENTION: No. 6472197a1 Grb2 Associating Protein and Nucleic  
; Acids Encoding Therefor  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/969,528  
; FILING DATE: 01-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/560,005  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 2307K-0624000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 976 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-969-528-2  
Query Match 0.6%; Score 8; DB 4; Length 976;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1075 TLPSLESL 1082  
14 TLPSLESL 21  
Db

ADDRESSER: MERCHANT & GOULD  
STREET: 3100 No. 6218162west Center, 90 South Seventh Street  
CITY: Minneapolis  
STATE: Minnesota  
COUNTRY: U.S.A.  
ZIP: 55402-4131  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/664,962B  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Douglas P.  
; REGISTRATION NUMBER: 30,300  
; REFERENCE/DOCKET NUMBER: MAG 7933.49-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1185 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-664-962B-2  
Query Match 0.6%; Score 8; DB 3; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1075 TLPSLESL 1082  
226 TLPSLESL 233  
Db

RESULT 35  
US-09-311-743-2  
; Sequence 2, Application US/09311743  
; Patent No. 6238903  
; GENERAL INFORMATION:  
; APPLICANT: Krysstal, Gerald  
; TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BERESKIN & PARR  
; STREET: 40 King Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/311,743  
; FILING DATE: 14-May-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gravelle, Michelle  
; REGISTRATION NUMBER: 40,261  
; REFERENCE/DOCKET NUMBER: 7771-32  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 416-364-7311  
; TELEFAX: 416-361-1398  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1185 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-311-743-2

Query Match 0.6%; Score 8; DB 3; Length 1185;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082  
DB 225 TLPSLESL 233

RESULT 36  
US-08-664-962B-8  
Sequence 8, Application US/08664962B  
Patent No. 6218162  
GENERAL INFORMATION:  
APPLICANT: Kiyetal, Gerald  
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MERCHANT & GOULD  
STREET: 3100 No. 6218162west Center, 90 South Seventh Street  
CITY: Minneapolis  
STATE: Minnesota  
COUNTRY: U.S.A.  
ZIP: 55402-4131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/664,962B  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueller, Douglas P.  
REGISTRATION NUMBER: 30,300  
REFERENCE/DOCKET NUMBER: McK 7933.49-US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-664-962B-8

Query Match 0.6%; Score 8; DB 3; Length 1187;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082  
DB 225 TLPSLESL 232

RESULT 37  
US-09-311-743-8  
Sequence 8, Application US/09311743  
Patent No. 6238903  
GENERAL INFORMATION:  
APPLICANT: Kiyetal, Gerald  
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/311,743  
FILING DATE: 14-May-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Gravelle, Micheline  
REGISTRATION NUMBER: 40,261  
REFERENCE/DOCKET NUMBER: 7771-32  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 416-364-7311  
TELEFAX: 416-361-1398  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-311-743-8

Query Match 0.6%; Score 8; DB 3; Length 1187;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLESL 1082  
DB 225 TLPSLESL 232

RESULT 38  
US-09-195-868-15  
Sequence 15, Application US/09195868  
Patent No. 6090621  
GENERAL INFORMATION:  
APPLICANT: KAVANAUGH MD, MICHAEL  
APPLICANT: POT PH.D., DAVID  
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/195,868  
FILING DATE:  
CLASSIFICATION:  
APPLICATION NUMBER: US/09/195,868  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FIRESTONE, LETCH H.  
REGISTRATION NUMBER: 36,831  
REFERENCE/DOCKET NUMBER: 1182.004  
TELECOMMUNICATION INFORMATION:



TELEPHONE: 510-923-2707  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1189 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-195-868-15

Query Match 0.6%; Score 8; DB 3; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSL 1082  
DB 227 TLPSL 234

RESULT 39  
US-09-195-868-28

Sequence 28, Application US/09195868  
Patent No. 6090621  
GENERAL INFORMATION:  
APPLICANT: KAVANAUGH MD, MICHAEL  
APPLICANT: POT PH.D., DAVID  
APPLICANT: WILLIAMS MDPH, LEWIS T.  
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE  
TITLE OF INVENTION: 5-PHOSPHATASES (SIPs)  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CHIRON CORPORATION  
STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/195,868  
FILING DATE:  
CLASSIFICATION:  
APPLICATION NUMBER: US/09/195,868  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FIRESTONE, LEIGH H.  
REGISTRATION NUMBER: 36,831  
REFERENCE/DOCKET NUMBER: 1182.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-923-2707  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-195-868-28

Query Match 0.6%; Score 8; DB 3; Length 1229;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSL 1082  
DB 267 TLPSL 274

RESULT 40  
US-09-515-514-15  
Sequence 15, Application US/09515514  
Patent No. 6509162  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: Methods for Selectively Modulating Survival Apoptosis  
TITLE OF INVENTION: Pathways  
FILE REFERENCE: 44574-5063-US  
CURRENT APPLICATION NUMBER: US/09/515,514  
CURRENT FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 15  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: NAIP phosphorylation motif  
US-09-515-514-15

Query Match 0.5%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 WIPOMA 82  
DB 1 WIPOMA 7

RESULT 41  
US-08-078-311-9

Sequence 9, Application US/08078311  
Patent No. 5925750  
GENERAL INFORMATION:  
APPLICANT: Charon, Martine  
APPLICANT: Gisselbrecht, Sylvie  
APPLICANT: Pencicelli, Jean-Francois  
APPLICANT: Souyri, Michele  
APPLICANT: Tambourin, Pierre  
APPLICANT: Varlet, Paule  
APPLICANT: Vigon, Isabelle  
TITLE OF INVENTION: polypeptide of a Growth Factor Receptor  
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 NO. 5925750west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/078,311  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NO PCT/FR90/00762  
FILING DATE: 19-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Katherine M.  
REGISTRATION NUMBER: 36,848  
REFERENCE/DOCKET NUMBER: 8076.84USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-078-311-9

Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 LSAALGL 29  
DB 11 LSAALGL 17

RESULT 42  
US-08-460-402-9  
Sequence 9, Application US/08460402  
Patent No. 598833  
GENERAL INFORMATION:  
APPLICANT: Charon, Martine  
APPLICANT: Gieselbrecht, Sylvie  
APPLICANT: Penciolelli, Jean-Francois  
APPLICANT: Souvri, Michele  
APPLICANT: Tambourin, Pierre  
APPLICANT: Varlet, Paule  
APPLICANT: Vison, Isabelle  
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor  
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of  
NUMBER OF INVENTIONS: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 598833west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,402  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/309,259  
FILING DATE: 20-SEP-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,311  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR90/00762  
FILING DATE: 14-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Randall A. Hillson  
REGISTRATION NUMBER: 31,838  
REFERENCE/DOCKET NUMBER: 8076,84US03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-402-9

Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 LSAALGL 29  
DB 11 LSAALGL 17

RESULT 43  
US-09-045-632-68  
Sequence 68, Application US/09045632  
Patent No. 6001575  
GENERAL INFORMATION:  
APPLICANT: Huganir, Richard L.  
APPLICANT: Dong, Hualing  
TITLE OF INVENTION: THERAPEUTIC USES OF GRIP AND  
NUMBER OF INVENTIONS: 105  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,632  
FILING DATE: 19-MAR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/041,016  
FILING DATE: 19-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Corlees, Peter F.  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 48147/1699-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-045-632-68

Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 578 LIAVATN 584  
DB 24 LIAVATN 30

RESULT 44  
US-08-176-500-71  
Sequence 71, Application US/08176500  
Patent No. 5498538  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/176,500  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/013,416  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-143  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-176-500-71

Query Match 0.5%; Score 7; DB 1; Length 38;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 SOVPTID 947  
Db 1 SOVPTID 7

RESULT 45  
US-08-471-052A-71  
Sequence 71, Application US/08471052A  
Patent No. 5625033  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
ADDRESSEE: Fowlkes, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,052A  
FILING DATE: 06-JUNE-1995  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-052A-71

Query Match 0.5%; Score 7; DB 1; Length 38;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 SOVPTID 947  
Db 1 SOVPTID 7

RESULT 46  
US-08-189-331-71  
Sequence 71, Application US/08189331  
Patent No. 5747334  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
ADDRESSEE: Fowlkes, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 186  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/189,331  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-189-331-71

Query Match 0.5%; Score 7; DB 1; Length 38;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 SOVPTID 947

Db 1 SOVPTID 7

## RESULT 47

US-08-471-939-71  
Sequence 71, Application US/08471939  
Patent No. 5844076  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
APPLICANT: Fowler, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,939  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/013,416  
FILING DATE: 01-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-143  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-939-71

## Query Match

Best Local Similarity 0.54; Score 7; DB 2; Length 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 SOVPTID 947  
Db 1 SOVPTID 7

## RESULT 48

US-08-471-800-71  
Sequence 71, Application US/08471800  
Patent No. 5852167  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
APPLICANT: Fowler, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,800  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/013,416  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-143  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-800-71

## Query Match

Best Local Similarity 0.54; Score 7; DB 2; Length 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 941 SOVPTID 947  
Db 1 SOVPTID 7

## RESULT 49

US-08-471-068-71  
Sequence 71, Application US/08471068  
Patent No. 5948635  
GENERAL INFORMATION:  
APPLICANT: Kay, B. K.  
APPLICANT: Fowler, D. M.  
TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
NUMBER OF SEQUENCES: 186  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,068  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/189,331  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-155  
TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-068-71

Query Match 0.5%; Score 7; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 SCVPTID 947  
Db 1 SCVPTID 7

RESULT 50  
US-08-569-749-9  
Sequence 9, Application US/08569749  
PATENT INFORMATION:  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-569-749-9

Query Match 0.5%; Score 7; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 BHAKMP 222  
Db 39 BHAKMP 45

RESULT 51  
PCT-US96-12860-9  
Sequence 9, Application PC/TUS9612860

GENERAL INFORMATION:  
APPLICANT: TULARIK, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-12860-9

Query Match 0.5%; Score 7; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 BHAKMP 222  
Db 39 BHAKMP 45

RESULT 52  
US-09-177-249-94  
Sequence 94, Application US/09177249  
PATENT INFORMATION:  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
FILE REFERENCE: 023070-086120US  
CURRENT APPLICATION NUMBER: US/09/177,249  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: US 09/071,838  
EARLIER FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 94  
LENGTH: 50  
TYPE: PRT

ORGANISM: Arabidopsis sp.  
us-09-177-249-94

## Query Match

Best Local Similarity 0.5%; Score 7; DB 3; Length 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 RLRKFMV 627  
DB 20 RLRKFMV 26

## RESULT 53

US-08-975-080-21  
Sequence 21, Application US/08975080  
Patent No. 6245523

GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,080  
FILING DATE: 20-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7176  
TELEFAX: 202-467-7000

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-975-080-21

Query Match  
Best Local Similarity 0.5%; Score 7; DB 3; Length 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKEFP 222  
DB 29 EHAKEFP 35

## RESULT 54

US-08-975-080-22  
Sequence 22, Application US/08975080  
Patent No. 6245523

GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869

## CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,080  
FILING DATE: 20-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7176  
TELEFAX: 202-467-7000

INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-975-080-22

Query Match  
Best Local Similarity 0.5%; Score 7; DB 3; Length 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKEFP 222  
DB 29 EHAKEFP 35

## RESULT 55

US-08-975-080-31  
Sequence 31, Application US/08975080  
Patent No. 6245523

GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,080  
FILING DATE: 20-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988

```

; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-975-080-31

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKWP 222
DB 29 EHAKWP 35

RESULT 56
US-08-511-485-23
; Sequence 23, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-511-485-23

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 PNCPL 345
DB 61 PNCPL 67
```

```

RESULT 57
US-09-201-936-23
; Sequence 23, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-23

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 PNCPL 345
DB 61 PNCPL 67

RESULT 58
US-08-511-485-27
; Sequence 27, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8306  
 TELE: 200154  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 68 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: both  
 MOLECULE TYPE: protein  
 US-08-511-485-27

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 68;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKWFP 222  
 DB 57 EHAKWFP 63

RESULT 59  
 US-09-201-936-27  
 Sequence 27, Application US/09201936  
 Patent No. 6541457  
 GENERAL INFORMATION:  
 APPLICANT: Korneluk, Robert G.  
 APPLICANT: MacKenzie, Alexander E.  
 APPLICANT: Lielon, Peter  
 TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
 FILE REFERENCE: 07861/003003  
 CURRENT APPLICATION NUMBER: US/09/201,936  
 EARLIER FILING DATE: 1998-12-01  
 EARLIER APPLICATION NUMBER: 09/011,356  
 EARLIER FILING DATE: 1998-02-04  
 EARLIER APPLICATION NUMBER: PCT/US96/01022  
 EARLIER FILING DATE: 1996-08-05  
 EARLIER APPLICATION NUMBER: 08/576,956  
 EARLIER FILING DATE: 1995-12-22  
 EARLIER APPLICATION NUMBER: 08/511,485  
 NUMBER OF SEQ ID NOS: 45  
 SOFTWARE: PaeSeq for Windows Version 3.0  
 SEQ ID NO 27  
 LENGTH: 68  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-201-936-27

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 4; Length 68;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKWFP 222  
 DB 57 EHAKWFP 63

RESULT 60  
 US-08-469-412A-14  
 Sequence 14, Application US/08469412A  
 Patent No. 656125  
 GENERAL INFORMATION:  
 APPLICANT: Mavrothalasitis, George J.  
 APPLICANT: Blair, Donald G.  
 APPLICANT: Fisher, Robert J.  
 APPLICANT: Beal Jr., Gregory J.  
 APPLICANT: Athanasiou, Merope A.  
 APPLICANT: Sgouras, Dionysios N.  
 TITLE OF INVENTION: The ERF Genetic Locus and Its Products  
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/469,412A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Garrett-Mackowski, Eugenia  
 REGISTRATION NUMBER: 37,330  
 REFERENCE/DOCKET NUMBER: 015280-229000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 81 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULAR TYPE: peptide  
 FEATURES:  
 NAME/KEY: Domain  
 LOCATION: 1..81  
 OTHER INFORMATION: /note= "an homologous region to  
 US-08-469-412A-14  
 OTHER INFORMATION: etc-1like ERF DNA-binding domain"

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 81;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 IOKNHL 573  
 DB 44 IOKNHL 50

RESULT 61  
 US-09-021-715-14  
 Sequence 14, Application US/09021715  
 Patent No. 6194547  
 GENERAL INFORMATION:  
 APPLICANT: Mavrothalasitis, George J.  
 APPLICANT: Blair, Donald G.  
 APPLICANT: Fisher, Robert J.  
 APPLICANT: Beal Jr., Gregory J.  
 APPLICANT: Athanasiou, Merope A.  
 APPLICANT: Sgouras, Dionysios N.  
 TITLE OF INVENTION: The ERF Genetic Locus and Its Products  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/021,715



FILING DATE: 10-Feb-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Mackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 015280-229000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Domain  
LOCATION: 1..81  
OTHER INFORMATION: /note="Yan homologous region to  
esr-like ERF DNA-binding domain"  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-021-715-14

Query Match 0.5%; Score 7; DB 3; Length 81;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 IOKNHL 573  
DB 44 IOKNHL 50

RESULT 62  
US-09-100-804-24  
Sequence 24, Application US/09100804  
Patent No. 6066472  
GENERAL INFORMATION:  
APPLICANT: GONZ, LEONEL JORGE  
APPLICANT: SARAS, JAN  
APPLICANT: CLAESON-WEISH, LENA  
APPLICANT: HELDIN, CARL-HENRIK  
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL  
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,804  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/596,291  
FILING DATE: 09-AUG-1996  
APPLICATION NUMBER: US 08/115,573  
FILING DATE: 01-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09943  
FILING DATE: 01-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: L0461/7003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-100-804-24

Query Match 0.5%; Score 7; DB 3; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 578 LIAVRTN 584  
DB 48 LIAVRTN 54

RESULT 63  
US-09-328-352-5481  
Sequence 5481, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5481  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5481

Query Match 0.5%; Score 7; DB 4; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AKRLKTF 67  
DB 105 AKRLKTF 111

RESULT 64  
US-09-328-352-5532  
Sequence 5532, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5532  
LENGTH: 139  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5532

Query Match 0.5%; Score 7; DB 4; Length 139;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AKRLKTF 67  
 |||||  
 DB 105 AKRLKTF 111

## RESULT 65

US-09-328-352-5595  
 ; Sequence 5595, Application US/09328352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 5595  
 ; LENGTH: 145  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter baumannii  
 US-09-328-352-5595

Query Match 0.5%; Score 7; DB 4; Length 145;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AKRLKTF 67  
 |||||  
 DB 105 AKRLKTF 111

## RESULT 66

US-09-328-352-5394  
 ; Sequence 5394, Application US/09328352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 5394  
 ; LENGTH: 152  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter baumannii  
 US-09-328-352-5394

Query Match 0.5%; Score 7; DB 4; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AKRLKTF 67  
 |||||  
 DB 105 AKRLKTF 111

## RESULT 67

US-09-738-946-4  
 ; Sequence 4, Application US/09738946  
 ; Patent No. 6579701  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EXELIXIS, INC.  
 ; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER  
 ; FILE REFERENCE: EX00-043C  
 ; CURRENT APPLICATION NUMBER: US/09/738,946  
 ; CURRENT FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 60/170,832  
 ; PRIOR FILING DATE: 1999-12-14

; PRIOR APPLICATION NUMBER: 60/170,838  
 ; PRIOR FILING DATE: 1999-12-14  
 ; PRIOR APPLICATION NUMBER: 60/178,580  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: 60/185,879  
 ; PRIOR FILING DATE: 2000-02-29  
 ; PRIOR APPLICATION NUMBER: 60/185,880  
 ; PRIOR FILING DATE: 2000-02-29  
 ; PRIOR APPLICATION NUMBER: 60/186,150  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 60/189,701  
 ; PRIOR FILING DATE: 2000-03-15  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 153  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-738-946-4

Query Match 0.5%; Score 7; DB 4; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 DDPWKEH 217  
 |||||  
 DB 84 DDPWKEH 90

## RESULT 68

US-09-328-352-7105  
 ; Sequence 7105, Application US/09328352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 7105  
 ; LENGTH: 159  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter baumannii  
 US-09-328-352-7105

Query Match 0.5%; Score 7; DB 4; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AKRLKTF 67  
 |||||  
 DB 105 AKRLKTF 111

## RESULT 69

US-08-034-245-14  
 ; Sequence 14, Application US/08034245  
 ; Patent No. 5504197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schubert, David  
 ; TITLE OF INVENTION: NEUROTROPIC GROWTH FACTOR AND METHODS  
 ; FILE REFERENCE: OF TREATMENT  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 ; STREET: 444 South Flower Street, Suite 2000  
 ; CITY: Los Angeles  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/034,245  
FILING DATE: 19930322  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,359  
FILING DATE: 27-SEP-1990  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/541,276  
FILING DATE: 20-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9369  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 181 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-034-245-14

Query Match 0.5%; Score 7; DB 1; Length 181;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEOKE 45  
DB 36 EEEEOKE 42

RESULT 70  
US-08-078-311-4  
Sequence 4, Application US/08078311  
Patent No. 5925750  
GENERAL INFORMATION:  
APPLICANT: Charon, Martine  
APPLICANT: Gisselbrecht, Sylvie  
APPLICANT: Penciolelli, Jean-Francios  
APPLICANT: Souyri, Michele  
APPLICANT: Tambourin, Pierre  
APPLICANT: Varlet, Paule  
APPLICANT: Vigon, Isabelle  
APPLICANT: Wendling, Francoise  
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor  
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of  
TITLE OF INVENTION: Myeloproliferative Disease  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Merchant & Gould  
STREET: 3100 No. 5925750west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/078,311  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR90/00762  
FILING DATE: 19-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalczyk, Katherine M.  
REGISTRATION NUMBER: 36,848  
REFERENCE/DOCKET NUMBER: 8076.84USWO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-078-311-4

Query Match 0.5%; Score 7; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LSNLGL 29  
DB 56 LSNLGL 62

RESULT 71  
US-08-460-402-4  
Sequence 4, Application US/08460402  
Patent No. 5989833  
GENERAL INFORMATION:  
APPLICANT: Charon, Martine  
APPLICANT: Gisselbrecht, Sylvie  
APPLICANT: Penciolelli, Jean-Francios  
APPLICANT: Souyri, Michele  
APPLICANT: Tambourin, Pierre  
APPLICANT: Varlet, Paule  
APPLICANT: Vigon, Isabelle  
APPLICANT: Wendling, Francoise  
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor  
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of  
TITLE OF INVENTION: Myeloproliferative Disease  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 5989833west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,402  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/309,259  
FILING DATE: 20-SEP-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,311  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR90/00762  
FILING DATE: 14-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Randall A. Hillson  
REGISTRATION NUMBER: 31,838

REFERENCE/DOCKET NUMBER: 8076.84US03  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEFAX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 184 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-460-402-4

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 184;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 LSAALGL 29  
 Db 56 LSAALGL 62

#### RESULT 72

US-09-328-352-7240  
 Sequence 7240, Application US/09328352  
 Patent No. 6562938

#### GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328.352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 7240  
 LENGTH: 189  
 TYPE: PRT  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-7240

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 AKRLKTF 67  
 Db 105 AKRLKTF 111

#### RESULT 73

US-08-188-582-24  
 Sequence 24, Application US/08188582  
 Patent No. 5534410

#### GENERAL INFORMATION:

APPLICANT: Tjian, Robert  
 APPLICANT: Comai, Lucio  
 APPLICANT: Dynlacht, Brian D.  
 APPLICANT: Hoey, Timothy  
 APPLICANT: Ruppert, Siegfried  
 APPLICANT: Tanese, Naoko  
 APPLICANT: Wang, Edith  
 APPLICANT: Weinzierl, Robert O.J.  
 TITLE OF INVENTION: YATA-BINDING PROTEIN ASSOCIATED FACTORS,  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/188,582  
 FILING DATE: 28-JAN-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277239

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 197 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-188-582-24

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 1; Length 197;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 KELESEE 42  
 Db 80 KELESEE 86

#### RESULT 74

US-08-646-715-24  
 Sequence 24, Application US/08646715  
 Patent No. 5637686

#### GENERAL INFORMATION:

APPLICANT: Tjian, Robert  
 APPLICANT: Comai, Lucio  
 APPLICANT: Dynlacht, Brian D.  
 APPLICANT: Hoey, Timothy  
 APPLICANT: Ruppert, Siegfried  
 APPLICANT: Tanese, Naoko  
 APPLICANT: Wang, Edith  
 APPLICANT: Weinzierl, Robert O.J.  
 TITLE OF INVENTION: YATA-BINDING PROTEIN ASSOCIATED FACTORS,  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,715  
 FILING DATE: 09-MAY-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/188,582  
 FILING DATE: 28-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-715-24

Query Match 0.5%; Score 7; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 KELEEE 42  
DB 80 KELEEE 86

RESULT 75  
US-09-134-001C-4407  
Sequence 4407, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: CTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4407  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4407

Query Match 0.5%; Score 7; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 NMTRLRK 624  
DB 196 NMTRLRK 202

Search completed: December 18, 2003, 09:16:06  
Job time : 27 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 ; Search time 76 Seconds  
(without alignments)  
4763.787 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403  
Sequence: 1 MATOQKASPERISQFDHNL.....SKYTLIQWLPFSPIIQ 1403

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: SPREMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1099	78.3	1160	4	Q8TD24
2	35	2.5	1271	11	Q8CH71
3	35	2.5	1432	11	Q8CGS9
4	35	2.5	1446	11	Q8CG17
5	35	2.5	1447	11	Q8CH66
6	35	2.5	1447	11	Q8CGT1
7	35	2.5	1447	11	Q8CGT0
8	35	2.5	1447	11	Q8CGS8
9	35	2.5	1447	11	Q8CGS7
10	26	1.9	1402	11	Q8CH65
11	26	1.9	1403	11	Q8CH70
12	24	1.7	1402	11	Q8CGT3
13	24	1.7	1402	11	Q8CGT4
14	24	1.7	1403	11	Q8CH68
15	24	1.7	1403	11	Q8CH64
16	24	1.7	1403	11	Q8CH64

17	24	1.7	1403	11	Q8CGT2	Q8CGT2 mus musculu
18	24	1.7	1403	11	Q8B6G8	Q8B6G8 mus musculu
19	23	1.6	1517	11	Q8A4U8	Q8A4U8 ratu mus norv
20	16	1.1	100	11	Q8CAX8	Q8CAX8 mus musculu
21	11	0.8	87	11	Q09123	Q09123 mus musculu
22	11	0.8	87	11	Q09120	Q09120 mus musculu
23	10	0.7	87	11	Q09119	Q09119 mus musculu
24	9	0.6	210	16	Q97PD4	Q97PD4 streptococc
25	9	0.6	241	17	Q8TP89	Q8TP89 methanosarc
26	9	0.6	349	11	Q8R2S2	Q8R2S2 mus musculu
27	9	0.6	349	11	Q9D5C4	Q9D5C4 mus musculu
28	9	0.6	349	11	Q8B2B3	Q8B2B3 mus musculu
29	9	0.6	350	4	Q9H5K3	Q9H5K3 homo sapien
30	9	0.6	360	6	Q95J00	Q95J00 macaca faec
31	9	0.6	414	10	Q91X22	Q91X22 arabidopsis
32	9	0.6	439	10	Q9FJ37	Q9FJ37 arabidopsis
33	9	0.6	469	10	Q8GUK8	Q8GUK8 arabidopsis
34	9	0.6	827	16	Q9HY15	Q9HY15 pseudomonas
35	8	0.6	74	2	Q9ZHW6	Q9ZHW6 brucei me
36	8	0.6	111	11	Q9WU86	Q9WU86 mus musculu
37	8	0.6	120	1	Q06500	Q06500 desulfuroco
38	8	0.6	146	17	Q9YDP1	Q9YDP1 aeropyrum p
39	8	0.6	147	16	Q9RSR8	Q9RSR8 deinococcus
40	8	0.6	151	5	Q81R03	Q81R03 dirosophila
41	8	0.6	152	17	Q30299	Q30299 archaeoglob
42	8	0.6	155	12	Q9YMI9	Q9YMI9 lymantria d
43	8	0.6	169	17	Q8ZU27	Q8ZU27 pyrobaculum
44	8	0.6	192	4	Q9Y329	Q9Y329 homo sapien
45	8	0.6	197	5	Q9VX87	Q9VX87 dirosophila
46	8	0.6	202	5	P91724	P91724 dirosophila
47	8	0.6	213	5	Q8WVNI	Q8WVNI bolitena vi
48	8	0.6	219	2	Q52735	Q52735 rhizobium e
49	8	0.6	219	16	Q8UC11	Q8UC11 agrobacteri
50	8	0.6	230	16	Q8XR2	Q8XR2 salmonella
51	8	0.6	232	10	Q8LB50	Q8LB50 arabidopsis
52	8	0.6	233	10	Q9LPE1	Q9LPE1 arabidopsis
53	8	0.6	253	11	Q922B4	Q922B4 ratu mus norv
54	8	0.6	253	11	Q9QY27	Q9QY27 mus musculu
55	8	0.6	253	11	Q9DD12	Q9DD12 mus musculu
56	8	0.6	268	13	Q9DGN3	Q9DGN3 gallus gall
57	8	0.6	307	16	Q8FLC0	Q8FLC0 escherichia
58	8	0.6	314	2	Q9X6W1	Q9X6W1 escherichia
59	8	0.6	315	16	Q98JF7	Q98JF7 rhizobium l
60	8	0.6	329	5	Q46012	Q46012 caenorhabdi
61	8	0.6	331	16	Q8XVS1	Q8XVS1 ralsronia s
62	8	0.6	343	17	Q93E95	Q93E95 enterococcu
63	8	0.6	345	17	Q57896	Q57896 pyrococcus
64	8	0.6	358	10	Q8LB55	Q8LB55 arabidopsis
65	8	0.6	358	10	Q82487	Q82487 arabidopsis
66	8	0.6	365	16	Q97H79	Q97H79 clostridium
67	8	0.6	372	16	Q92NG8	Q92NG8 rhizobium m
68	8	0.6	372	16	Q8DT00	Q8DT00 streptococc
69	8	0.6	390	16	Q98DC3	Q98DC3 rhizobium l
70	8	0.6	391	16	Q54143	Q54143 streptomyc
71	8	0.6	396	5	Q04151	Q04151 toxoplasma
72	8	0.6	401	13	Q8LHV9	Q8LHV9 xenopus lae
73	8	0.6	422	17	Q9V1G6	Q9V1G6 pyrococcus
74	8	0.6	429	16	Q98C86	Q98C86 rhizobium l
75	8	0.6	437	16	Q98C91	Q98C91 rhizobium l
76	8	0.6	470	2	Q8RNP3	Q8RNP3 legionella
77	8	0.6	489	16	Q8FCZ4	Q8FCZ4 escherichia
78	8	0.6	496	11	Q9ERS0	Q9ERS0 ratu mus norv
79	8	0.6	501	11	Q9BD04	Q9BD04 ratu mus norv
80	8	0.6	501	11	Q9BD05	Q9BD05 ratu mus norv
81	8	0.6	521	5	Q9VTP9	Q9VTP9 dirosophila
82	8	0.6	532	11	Q9QY28	Q9QY28 mus musculu
83	8	0.6	538	5	Q9VGB6	Q9VGB6 dirosophila
84	8	0.6	575	5	Q9VGS5	Q9VGS5 dirosophila
85	8	0.6	654	10	Q9ZTW9	Q9ZTW9 oryza sativ
86	8	0.6	656	10	Q9ZTX2	Q9ZTX2 ipomoea bat
87	8	0.6	657	10	Q94C06	Q94C06 ipomoea bat
88	8	0.6	671	4	Q95559	Q95559 homo sapien
89	8	0.6	679	5	Q9VJ15	Q9VJ15 dirosophila

90 8 0.6 679 5 Q2185  
91 8 0.6 682 10 Q94C08  
92 8 0.6 803 16 Q981S5  
93 8 0.6 837 11 Q63618  
94 8 0.6 840 10 Q81PM3  
95 8 0.6 845 4 Q944Q0  
96 8 0.6 854 4 Q9H0A2  
97 8 0.6 871 11 Q9ET47  
98 8 0.6 926 10 Q81GNO  
99 8 0.6 934 10 Q81080  
100 8 0.6 959 11 Q9UKR7

## ALIGNMENTS

Q2185 drosophila  
Q94C08 oryza sativ  
Q981S5 rhizobium 1  
Q63618 ractus novy  
Q81PM3 citreus hybr  
Q944Q0 homo sapien  
Q9H0A2 homo sapien  
Q9ET47 mus musculu  
Q81GNO arabidopsis  
Q81080 arabidopsis  
Q9UKR7 mus musculu

## RESULT 1

Q8TDZ4 PRELIMINARY; PRT; 1160 AA.  
AC 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
GN Psi neuronal apoptosis inhibitory protein (fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Xu M., Okada T., Sakai H., Miyamoto N., Yanagisawa Y., Mackenzie A.E.,  
RT "Functional human Naip promoter and transcriptional regulatory  
RT elements for the human Naip and psinaip genes."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBS databases.  
DR EMBL; AB048534; BAB87181.1; -  
DR InterPro; IPR001370; AAA\_ATPase.  
DR InterPro; IPR007111; NACHT\_NTPase.  
DR Pfam; PF00653; BIR\_1.  
DR SMART; SM00382; AAA\_1.  
DR SMART; SM00388; BIR\_1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 1.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 1.  
DR ATP-Binding; PS0837; NACHT; 1.  
KW ATP-binding.  
FT NON\_TER  
SQ SEQUENCE 1160 AA; 131893 MW; 78C947C93A4F5876 CRC64;

Query Match 78.3%; Score 1099; DB 4; Length 1160;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 CEFPLRSKSSSEITQYQSYKGFVDITGEHFVNSWQRELPMAASAYCNDISFAVEELRLD 283  
Db 62 CEFPLRSKSSSEITQYQSYKGFVDITGEHFVNSWQRELPMAASAYCNDISFAVEELRLD 283  
QY 284 SFKDMPRESAVGVAALAKAGLFTYGIKDIYVOCFSCGCLCEKMOGSDDDLDRHTCPNCP 343  
Db 122 SFKDMPRESAVGVAALAKAGLFTYGIKDIYVOCFSCGCLCEKMOGSDDDLDRHTCPNCP 343  
QY 344 FLONMSSASAVTPDLOSRELCELETTSESULESTAVGIVPEMAQGEAOWFOEAKYL 403  
Db 182 FLONMSSASAVTPDLOSRELCELETTSESULESTAVGIVPEMAQGEAOWFOEAKYL 403  
QY 404 NEOLRAAYASFRHMSLIDSSDLATPHLIGCLSLASIKHISKPVOEPLVPEVGNIN 241  
Db 242 NEOLRAAYASFRHMSLIDSSDLATPHLIGCLSLASIKHISKPVOEPLVPEVGNIN 241  
QY 464 SYMCVEGAGSGKTYLLKKAIFLWASGCCPLNRFOLVFLSLSTRPDEGLASITCDQL 523  
Db 302 SYMCVEGAGSGKTYLLKKAIFLWASGCCPLNRFOLVFLSLSTRPDEGLASITCDQL 523

QY 524 LEKESGVTEMCRNRTIIQOLKNQVFLDDYVEICISIPQVIGKLIQKNHLSRTGLIANT 583  
Db 362 LEKESGVTEMCRNRTIIQOLKNQVFLDDYVEICISIPQVIGKLIQKNHLSRTGLIANT 583  
QY 584 NNAPIRREYLTETLEIKAFPPYNTVCILRLFGHNTMRIRKPMVYGGKQSLQKTPLE 643  
Db 422 NNAPIRREYLTETLEIKAFPPYNTVCILRLFGHNTMRIRKPMVYGGKQSLQKTPLE 643  
QY 644 FVAALCAHFPYPPDPSFDVAVFKSMRSLIRKATLEILKATVSSCGELALKGFPSC 703  
Db 482 FVAALCAHFPYPPDPSFDVAVFKSMRSLIRKATLEILKATVSSCGELALKGFPSC 703  
QY 704 CFEFNDDDLAAGVDEDEITWCLMSKPTAORLAPFRFLSPAPOEPLAGRLLELDSO 763  
Db 542 CFEFNDDDLAAGVDEDEITWCLMSKPTAORLAPFRFLSPAPOEPLAGRLLELDSO 763  
QY 764 ROEHODLGLYHLKOINSPMWTSAYNNFLANYVSSLPTKAGPKIVSHLHVDNKESLEN 823  
Db 602 ROEHODLGLYHLKOINSPMWTSAYNNFLANYVSSLPTKAGPKIVSHLHVDNKESLEN 823  
QY 824 ISENDDYLKHOPEISLOMLRGLWQICPOAYFMSVSEHLVTLATAYOSNTVAACSPF 883  
Db 662 ISENDDYLKHOPEISLOMLRGLWQICPOAYFMSVSEHLVTLATAYOSNTVAACSPF 883  
QY 884 VLOPLQGRITLIGALINQYFPDHPESLSLRSHFPIRGKTSPPRAHPSVLTCEPKSQV 943  
Db 722 VLOPLQGRITLIGALINQYFPDHPESLSLRSHFPIRGKTSPPRAHPSVLTCEPKSQV 943  
QY 944 PTIDODVASAFEPNWEERNLAKEENYKSYNDMQRASPDLSGTWKLSPKQYKIPCLE 1003  
Db 782 PTIDODVASAFEPNWEERNLAKEENYKSYNDMQRASPDLSGTWKLSPKQYKIPCLE 1003  
QY 1004 VDNDIDIVGQDMLEIMTYTFSASORIELHNSGPFESTIRPLELSEKASVTGCSISK 1063  
Db 842 VDNDIDIVGQDMLEIMTYTFSASORIELHNSGPFESTIRPLELSEKASVTGCSISK 1063  
QY 1064 ELSSAEGELLTLPSLESLEVGSTIOSODOI PPNDKELCLKEISVDLEGNINVSIVPE 901  
Db 902 ELSSAEGELLTLPSLESLEVGSTIOSODOI PPNDKELCLKEISVDLEGNINVSIVPE 901  
QY 1124 EFPNFMHEKLLIOISAEVDSKLVKLIQNSPNLHVHLKCNFPSPDGSIMTVLSCCKL 1183  
Db 962 EFPNFMHEKLLIOISAEVDSKLVKLIQNSPNLHVHLKCNFPSPDGSIMTVLSCCKL 1183  
QY 1184 TELKSDSPFOAVPFVASLPNFIKLITLNEGGQFPDESEKFAVILGSLNLELILP 1243  
Db 1022 TELKSDSPFOAVPFVASLPNFIKLITLNEGGQFPDESEKFAVILGSLNLELILP 1243  
QY 1244 TGDGIYVAKLIIOCCOHLCLVLSFRTLNDSDVVEIAKVAISGFOKLENKLSINH 1303  
Db 1082 TGDGIYVAKLIIOCCOHLCLVLSFRTLNDSDVVEIAKVAISGFOKLENKLSINH 1303  
QY 1304 KITEGYNRFQALDNMPN 1322  
Db 1142 KITEGYNRFQALDNMPN 1160

## RESULT 2

Q8CH71 PRELIMINARY; PRT; 1271 AA.  
AC 08CH71;  
DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DE Baculoviral IAP repeat-containing 1b (fragment).  
GN BIRCB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.



RC STRAIN=A/J;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endritzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.,  
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila,"  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL, AF367966; AAN77613.1;  
 DR EMBL, AF367966; AAN77613.1;  
 FT NON TER 1271 1271  
 SQ SEQUENCE 1271 AA; 144021 MW; 76213AEC741C3BE CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1271;  
 Best Local Similarity 100.0%; Pred. No. 66-26;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227  
 Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 3  
 ID 08CGS9 PRELIMINARY; PRT; 1432 AA.  
 AC 08CGS9;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Neuronal apoptosis inhibitory protein 2 (Fragment).  
 GN BIRCIB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cJ;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endritzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.,  
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila,"  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL, AY147002; AAN77586.1;  
 FT NON TER 1 1  
 SQ SEQUENCE 1432 AA; 162454 MW; 55DBE61FD6DE7FD CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1432;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-26;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227  
 Db 178 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 212

RESULT 4  
 ID 08CG17 PRELIMINARY; PRT; 1446 AA.  
 AC 08CG17;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Neuronal apoptosis inhibitory protein 2.  
 GN NAIIP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endritzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,

RA Dietrich W.F.;  
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila,"  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL, AF367967; AAN77615.1;  
 DR EMBL, AF367969; AAN77615.1; JOINED.  
 DR EMBL, AF367968; AAN77615.1; JOINED.  
 SQ SEQUENCE 1446 AA; 164012 MW; D566E810AF0B0A33 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1446;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-26;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227  
 Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 5  
 ID 08CH66 PRELIMINARY; PRT; 1447 AA.  
 AC 08CH66;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE BIRCIB protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/J; TISSUE=Spleen;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endritzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.,  
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila,"  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL, AF381770; AAN77911.1;  
 FT NON TER 1447 1447  
 SQ SEQUENCE 1447 AA; 163998 MW; 0EC3C0B7396E4298 CRC64;

Query Match 2.5%; Score 35; DB 11; Length 1447;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-26;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227  
 Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMPKCEFL 227

RESULT 6  
 ID 08CGT1 PRELIMINARY; PRT; 1447 AA.  
 AC 08CGT1;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Neuronal apoptosis inhibitory protein 2.  
 GN BIRCIB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129S1;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endritzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.,  
 RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila,"  
 RL Curr. Biol. 0:0-0(2003).

DR EMBL: AY147000; AAN7584.1; -  
SQ SEQUENCE 1447 AA; 16406 MW; 5EC277AA27169E02 CRC64;

Query Match

Best Local Similarity 2.5%; Score 35; DB 11; Length 1447;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227  
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227

RESULT 7  
08CGT0 PRELIMINARY; PRT; 1447 AA.

ID 08CGT0  
AC 08CGT0;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Neuronal apoptosis inhibitory protein 2.  
GN BIRC1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
RA Dietrich W.F.;  
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
RT Legionella pneumophila.";  
RL Curr. Biol. 0:0-0(2003).  
DR EMBL: AY147001; AAN7585.1; -  
SQ SEQUENCE 1447 AA; 16406 MW; 8C44045962AF54B CRC64;

Query Match

Best Local Similarity 2.5%; Score 35; DB 11; Length 1447;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227  
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227

RESULT 8

ID 08CGS8 PRELIMINARY; PRT; 1447 AA.

AC 08CGS8;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DE Neuronal apoptosis inhibitory protein 2.  
GN BIRC1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/HeJ;  
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
RA Dietrich W.F.;  
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
RT Legionella pneumophila.";  
RL Curr. Biol. 0:0-0(2003).  
DR EMBL: AY147003; AAN7587.1; -  
SQ SEQUENCE 1447 AA; 16410 MW; 4BF1679B1F582CF9 CRC64;

Query Match

Best Local Similarity 2.5%; Score 35; DB 11; Length 1447;  
Matches 100.0%; Pred. No. 6.7e-26;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227  
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227

RESULT 9

ID 08CGS7 PRELIMINARY; PRT; 1447 AA.

AC 08CGS7;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Neuronal apoptosis inhibitory protein 2.  
GN BIRC1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N;  
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
RA Dietrich W.F.;  
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
RT Legionella pneumophila.";  
RL Curr. Biol. 0:0-0(2003).  
DR EMBL: AY147004; AAN7588.1; -  
SQ SEQUENCE 1447 AA; 16410 MW; FA5489BCA5BDD CRC64;

Query Match

Best Local Similarity 2.5%; Score 35; DB 11; Length 1447;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227  
Db 193 DTVOCFSCGCGCLGNWEGDDPMKEHAKMFPKCEFL 227

RESULT 10

ID 08CH65 PRELIMINARY; PRT; 1402 AA.

AC 08CH65;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DE BIRC1B protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J; TISSUE=Spleen;  
RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
RA Dietrich W.F.;  
RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen  
RT Legionella pneumophila.";  
RL Curr. Biol. 0:0-0(2003).  
DR EMBL: AF381771; AAN7912.1; -  
SQ SEQUENCE 1402 AA; 159678 MW; 0BA0855BF40B55FD CRC64;

Query Match

Best Local Similarity 1.9%; Score 26; DB 11; Length 1402;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 483 IAFWASGCGCLNRFQVFTLSLS 508  
Db 483 IAFWASGCGCLNRFQVFTLSLS 508

## RESULT 11

Q8CH70

ID 08CH70 PRELIMINARY; PRT; 1403 AA.

AC 08CH70; 01-MAR-2003 (TEMBLrel. 23, Created)

DT 01-MAR-2003 (TEMBLrel. 23, last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, last annotation update)

DE Baculoviral IAP repeat-containing 1e.

GN BIRCIE

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A/J;

RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,

RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,

RA Dietrich W.F.;

RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen

RT Legionella pneumophila."

RL Curr. Biol. 0:0-0(2003).

DR EMBL; AF67966; AAN7612.1; "

SQ SEQUENCE 1403 AA; 159748 MW; 3237EICE2EAA06EF CRC64;

Query Match 1.7%; Score 24; DB 11; Length 1403;

Best Local Similarity 100.0%; Pred. No. 1.1e-16;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 483 IAFMASGCCPLNRFQVLYLSLS 508

DB 483 IAFMASGCCPLNRFQVLYLSLS 508

## RESULT 12

Q9R015

ID Q9R015 PRELIMINARY; PRT; 597 AA.

AC Q9R015; 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TEMBLrel. 13, last sequence update)

DT 01-OCT-2002 (TEMBLrel. 22, last annotation update)

DE Neuronal apoptosis inhibitory protein.

GN BIRCIE OR NAIP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99431676; PubMed=10501978;

RT "The mouse naip gene cluster on chromosome 13 encodes several distinct

RT functional transcripts."

RL Mamm. Genome 10:1032-1035(1999).

DR EMBL; AF135493; AADS6765.1; "

DR HSSP; Q13490; 10BH.

DR MGD; MGI:1298220; Bircie.

DR InterPro; IPR001370; BIR.

DR InterPro; IPR003892; CUE.

DR Pfam; PF00653; BIR; 3.

DR Pfam; PF02845; CUE; 1.

DR SMART; SM00238; BIR; 3.

DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.

DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.

SQ SEQUENCE 597 AA; 68322 MW; 404283E51A7F9A0 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 597;

Best Local Similarity 100.0%; Pred. No. 5.6e-15;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 LGNMBGDDPWKEHAKWPKCEFL 227

Q8CH68

DB 158 LGNMBGDDPWKEHAKWPKCEFL 181

## RESULT 13

Q8CGT4

ID Q8CGT4 PRELIMINARY; PRT; 1402 AA.

AC Q8CGT4; 01-MAR-2003 (TEMBLrel. 23, Created)

DT 01-MAR-2003 (TEMBLrel. 23, last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, last annotation update)

DE Neuronal apoptosis inhibitory protein 5.

GN BIRCIE

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129S1;

RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,

RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,

RA Dietrich W.F.;

RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen

RT Legionella pneumophila."

RL Curr. Biol. 0:0-0(2003).

DR EMBL; AY146994; AAN60206.1; "

SQ SEQUENCE 1402 AA; 159584 MW; E8B6C6CA3BF5F372 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 1402;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 LGNMBGDDPWKEHAKWPKCEFL 227

DB 204 LGNMBGDDPWKEHAKWPKCEFL 227

## RESULT 14

Q8CGT3

ID Q8CGT3 PRELIMINARY; PRT; 1402 AA.

AC Q8CGT3; 01-MAR-2003 (TEMBLrel. 23, Created)

DT 01-MAR-2003 (TEMBLrel. 23, last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, last annotation update)

DE Neuronal apoptosis inhibitory protein 5.

GN BIRCIE

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,

RA Endrizzi M.G., Long E.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,

RA Dietrich W.F.;

RT "Naip5 Affects Host Susceptibility to the Intracellular Pathogen

RT Legionella pneumophila."

RL Curr. Biol. 0:0-0(2003).

DR EMBL; AY146995; AAN60207.1; "

SQ SEQUENCE 1402 AA; 159768 MW; A04C55D45F4B3392 CRC64;

Query Match 1.7%; Score 24; DB 11; Length 1402;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 LGNMBGDDPWKEHAKWPKCEFL 227

DB 204 LGNMBGDDPWKEHAKWPKCEFL 227

## RESULT 15

Q8CH68

ID 08CH68 PRELIMINARY; PRT; 1403 AA.  
 AC 08CH68;  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DE Neuronal apoptosis inhibitory protein 6.  
 GN NAIP6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endrizzi M.G., Long B.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.;  
 RT "Naip6 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila.";  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL; AF367969; AAN77617.1;  
 SO SEQUENCE 1403 AA; 15985 MW; ABEF1450334FC2E7 CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 LGNMBGDDPWKEHAKMPKCEFL 227  
 DB 204 LGNMBGDDPWKEHAKMPKCEFL 227

RESULT 16  
 ID 08CH64 PRELIMINARY; PRT; 1403 AA.  
 AC 08CH64;  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DE Birc1f protein.  
 GN Birc1f protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/J; Tissue=Spleen;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endrizzi M.G., Long B.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.;  
 RT "Naip6 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila.";  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL; AF381772; AAN77913.1;  
 SO SEQUENCE 1403 AA; 15984 MW; 763C19EAP10AA37A CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 LGNMBGDDPWKEHAKMPKCEFL 227  
 DB 204 LGNMBGDDPWKEHAKMPKCEFL 227

RESULT 17  
 ID 08CGT2 PRELIMINARY; PRT; 1403 AA.  
 AC 08CGT2;  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DE Neuronal apoptosis inhibitory protein 5.  
 GN NAIP.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GN Birc1f.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P/J;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endrizzi M.G., Long B.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.;  
 RT "Naip6 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila.";  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL; AY146999; AAN60210.1;  
 SO SEQUENCE 1403 AA; 15985 MW; 04C04877908103BE CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 LGNMBGDDPWKEHAKMPKCEFL 227  
 DB 204 LGNMBGDDPWKEHAKMPKCEFL 227

RESULT 18  
 ID 08BG68 PRELIMINARY; PRT; 1403 AA.  
 AC 08BG68;  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DE Neuronal apoptosis inhibitory protein 5.  
 GN Birc1f.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cJ, C3H/HeJ, and FVB/N;  
 RA Wright E.K. Jr., Goodart S.A., Growney J.D., Hadinoto V.,  
 RA Endrizzi M.G., Long B.M., Sadigh K., Abney A.L., Bernstein-Hanley I.,  
 RA Dietrich W.F.;  
 RT "Naip6 Affects Host Susceptibility to the Intracellular Pathogen  
 RT Legionella pneumophila.";  
 RL Curr. Biol. 0:0-0(2003).  
 DR EMBL; AY146996; AAN60208.1;  
 DR EMBL; AY146997; AAN60209.1;  
 DR EMBL; AY146998; AAN60210.1;  
 SO SEQUENCE 1403 AA; 15986 MW; BD08B13D167BBF64 CRC64;

Query Match  
 Best Local Similarity 1.7%; Score 24; DB 11; Length 1403;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 LGNMBGDDPWKEHAKMPKCEFL 227  
 DB 204 LGNMBGDDPWKEHAKMPKCEFL 227

RESULT 19  
 ID 08R4U8 PRELIMINARY; PRT; 517 AA.  
 AC 08R4U8;  
 DT 01-JUN-2002 (TRENBLREL. 21, Created)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)  
 DE Neuronal apoptosis inhibitory protein (fragment).  
 GN NAIP.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Shin S.W., Park J.W., Lee M.Y., Yoo M., Kim S.K., Oh T.H., Choe B.K.;
RT "Molecular Cloning and Expression of Rat Neuronal Apoptosis Inhibitory
  Protein (NAIP).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361881; AAL99667.1; -.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR007111; NACHT_NTPase.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
DR PROSITE; PS50837; NACHT; 1.
FT NON_TER 1
FT 517 517
SQ SEQUENCE 517 AA; 58066 MW; 7BD2F80A2037D9C2 CRC64;

Query Match
Best Local Similarity 1.6%; Score 23; DB 11; Length 517;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 484 AELMASGCCPLNRFQVFLSL 506
DB 268 AELMASGCCPLNRFQVFLSL 290

RESULT 20
OBCAX8 PRELIMINARY; PRT; 100 AA.
AC 08CAX8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Baculoviral IAP repeat-containing 1e (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
  Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK037418; BAC29803.1; -.
FT NON_TER 1
FT 1
SQ SEQUENCE 100 AA; 11681 MW; 621A21C7542ECF8 CRC64;

Query Match
Best Local Similarity 1.1%; Score 16; DB 11; Length 100;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1304 KITBEGYRNFPQALDN 1319
DB 1 KITBEGYRNFPQALDN 16

RESULT 21
O09123 PRELIMINARY; PRT; 87 AA.
AC 009123;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE BACULOVIRAL IAP repeat-containing protein 1C (Neuronal apoptosis
  inhibitory protein, related sequence 5) (Fragment).

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GN BIRC1C OR NAIP3 OR NAIP-RS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Schaf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
  within the 1gnt critical interval and contains multiple copies of Naip
  exon 5.";
RL Genomics 38:405-417 (1996).
CC -1- SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
  APOPTOSIS PROTEIN REPEAT).
DR EMBL; U66325; AAC52976.1; -.
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298225; Birc1c.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
FT NON_TER 1
FT 87 87
SQ SEQUENCE 87 AA; 9997 MW; B164943B3BC52E3A CRC64;

Query Match
Best Local Similarity 0.8%; Score 11; DB 11; Length 87;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 QCFCCSLIFG 106
DB 15 QCFCCSLIFG 25

RESULT 22
O09120 PRELIMINARY; PRT; 87 AA.
AC 009120;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE BACULOVIRAL IAP repeat-containing protein 1D (Neuronal apoptosis
  inhibitory protein, related sequence 2) (Fragment).
GN BIRC1D OR NAIP4 OR NAIP-RS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=97131520; PubMed=8975718;
RA Schaf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
  within the 1gnt critical interval and contains multiple copies of Naip
  exon 5.";
RL Genomics 38:405-417 (1996).
CC -1- SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
  APOPTOSIS PROTEIN REPEAT).
DR EMBL; U66325; AAC52976.1; -.
DR HSSP; Q13490; 1QBH.
DR MGD; MGI:1298225; Birc1c.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE; PS50143; BIR_REPEAT_2; 1.
FT NON_TER 1
FT 1

```

FT NON\_TER 87 87  
SQ SEQUENCE 87 AA; 9972 MW; 9C34CD8224E71325 CRC64;

Query Match  
Best Local Similarity 0.8%; Score 11; DB 11; Length 87;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 QCFCCSLIFG 106  
DB 15 QCFCCSLIFG 25

## RESULT 23

ID 009119 PRELIMINARY; PRT; 87 AA.

AC 009119; PRT; 87 AA.  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DE Neutroal apoptosis inhibitory protein related sequence 1  
GN (Fragment)  
OS BIRCI-RS1 OR NAIP-RS1.  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN NCBI\_TaxId=10990;  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVJ;  
RX MEDLINE=97151520; PubMed=8975718;  
RA Schart J.M., Damron D., Frielella A., Bruno S., Beggs A.H.,  
RT Kunkel L.M., Dietrich W.F.;  
RT "The mouse region syntenic for human spinal muscular atrophy lies  
RT within the 1gln critical interval and contains multiple copies of Naip  
RT exon 5.";  
RL Genomics 38:405-417(1996).  
DR EMBL; U66324; AAC52972.1; -.  
DR HSSP; 013480; 10BH.  
DR MGD; MGI:109439; Birc1-rs1.  
DR InterPro; IPR001370; BIR.  
DR Pfam; PF00653; BIR.1.  
DR SMART; SM00238; BIR.1.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 87  
SQ SEQUENCE 87 AA; 9958 MW; E601604230BC1D25 CRC64;

Query Match  
Best Local Similarity 0.7%; Score 10; DB 11; Length 87;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 QCFCCSLIFG 105  
DB 15 QCFCCSLIFG 24

## RESULT 24

ID 097PD4 PRELIMINARY; PRT; 210 AA.

AC 097PD4; PRT; 210 AA.  
DT 01-OCT-2001 (T-EMBLrel. 18, Created)  
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)  
DE ABC transporter, ATP-binding protein.  
GN SP1704.  
OS Streptococcus pneumoniae.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxId=1313;  
RP SEQUENCE FROM N.A.  
RC STRAIN=TTGR4;  
RX MEDLINE=21357209; PubMed=11463916;

RA Tetterlin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
RA Peterson S., Heidelberg J., DeBoy R.T., Hatt D.H., Dodson R.J.,  
RA Durkin A.S., Gwinn M., Kolonay J.F., Lapid D.H., Peterson R.J.,  
RA Umayam L.A., White O., Salzberg S.L., Nelson W.C., Peterson J.D.,  
RA Holtzapple E., Khouri H., Wolf A.M., Lewis M.R., Radune D.,  
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hansen C.L.,  
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Hickey E.K.,  
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Frazer C.M.,  
RT "Complete genome sequence of a virulent isolate of Streptococcus  
RT pneumoniae.";  
RL Science 293:498-506(2001).  
DR EMBL; AE007463; AAK75782.1; -.  
DR TIGR; SP1704; -.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR SMART; SM00362; AAA; 1.  
KW ATP-binding; Complete proteome.  
SQ SEQUENCE 210 AA; 24022 MW; 41AB24DE1F6397E3 CRC64;

Query Match  
Best Local Similarity 0.6%; Score 9; DB 16; Length 210;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 473 GSGKTVLTK 481  
DB 38 GSGKTVLTK 46

## RESULT 25

ID 08TP89 PRELIMINARY; PRT; 241 AA.

AC 08TP89; PRT; 241 AA.  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
DE Predicted protein.  
GN MA2025.  
OS Methanosarcina acetivorans.  
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
OC Methanosarcinaceae; Methanosarcina.  
OX NCBI\_TaxId=2214;  
RP SEQUENCE FROM N.A.  
RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
RX MEDLINE=21929760; PubMed=11932238;  
RA Galagan J.E., Nusbaum C., Roy A.,  
RA Fitzhugh W., Calvo S., Engels R.,  
RA Allen N., Naylor J., Stange-Thomann N., DeAvaliano K., Johnson R.,  
RA Linton L., McMan P., McKernan K., Talamas D.E., Graham D.A., Guss A.M.,  
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Johnson R.,  
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Graham D.A., Guss A.M.,  
RA Leigh J.A., Li W., Liu V., Mukhopadhyay B., Reeve J.N., Smith K.,  
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic  
RT and physiological diversity.";  
RL Genome Res. 12:532-542(2002).  
DR EMBL; AE010888; AAM05426.1; -.  
KW Complete proteome.  
SQ SEQUENCE 241 AA; 27588 MW; 0BB9051BD3B32701 CRC64;

Query Match  
Best Local Similarity 0.6%; Score 9; DB 17; Length 241;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 815 VDNKSTLEN 823  
DB 165 VDNKSTLEN 173

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RESULT 26
Q8R2S2 PRELIMINARY; PRT; 349 AA.
AC Q8R2S2;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RIKEN CDNA 493044A02Rik.
GN 493044A02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027296; AAH27296.1; -
DR MGD; MGI:1921903; 493044A02Rik.
DR InterPro; IPR000719; Prot. Kinase.
DR Prodom; PD000001; Prot. Kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 349 AA; 39982 MW; 527DEE1017DB2E12 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 11; Length 349;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 LGSLSNLEE 1239
DB 153 LGSLSNLEE 161

RESULT 27
Q9D5G4 PRELIMINARY; PRT; 349 AA.
AC Q9D5G4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 493044A02Rik protein (Hypotheical eukaryotic protein kinase
DE containing protein).
GN 493044A02Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka R.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saio R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohenki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RN [2]

```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK015374; BAB29817.1; -
DR EMBL; AK036277; BAC27984.1; -
DR EMBL; AK043620; BAC31598.1; -
DR MGD; MGI:1921903; 493044A02Rik.
DR InterPro; IPR000719; Prot. Kinase.
DR Pfam; PF000069; pkinase; 1.
DR Prodom; PD000001; Prot. Kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 349 AA; 39968 MW; 0E8683A6DBA8A59C3 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 11; Length 349;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 LGSLSNLEE 1239
DB 153 LGSLSNLEE 161

RESULT 28
Q8B283 PRELIMINARY; PRT; 349 AA.
AC Q8B283;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical eukaryotic protein kinase containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK036348; BAC29393.1; -
KW Hypothetical protein.
SQ SEQUENCE 349 AA; 39995 MW; FF2C9207C5EB028D CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 11; Length 349;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 LGSLSNLEE 1239
DB 153 LGSLSNLEE 161

RESULT 29
Q9H5K3 PRELIMINARY; PRT; 350 AA.
AC Q9H5K3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ233356.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [2]

```

NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Kawabata A., Hiki J., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,  
 RA Tanaka T., Nakamura Y., Isonaga T., Sugano S.,  
 RL "NEBO human cDNA sequencing project."  
 DR Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027009; BAB15623.1;  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR Pfam: PF00069; Kinase; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 SO SEQUENCE 350 AA; 40050 MW; E074FDB2E5861B0F CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 9; DB 4; Length 350;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1231 LGSLNLEE 1239  
 154 LGSLNLEE 162

RESULT 30  
 ID 095J00 PRELIMINARY; PRT; 360 AA.  
 AC 095J00:  
 DT 01-DEC-2001 (TEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Hypothetical 41.3 kDa protein.  
 OS Macaca fascicularis (Orangutan macaque)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC Tissue:Testis;  
 RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,  
 RA Terao K., Sugano S.,  
 RT "Isolation of novel full-length cDNA clones from macaque testis cDNA  
 RT libraries."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB070191; BAB61336.1;  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR Pfam: PF00069; Kinase; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 KW Hypothetical protein; ATP-binding; Transferase.  
 SO SEQUENCE 360 AA; 41271 MW; 0697CDN00F34D098 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 9; DB 6; Length 360;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1231 LGSLNLEE 1239  
 164 LGSLNLEE 172

RESULT 31  
 ID 09LX22 PRELIMINARY; PRT; 414 AA.  
 AC 09LX22:  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Hypothetical 45.6 kDa protein.  
 OS Arabidopsis thaliana (Mouse-ear cress)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Zimmermann W., Gruenleisen A., Wambutt R., Kalicki J.,  
 RA Woldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,  
 RA Mayer K.F.X.,  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL356333; CAB92047.1;  
 DR InterPro: IPR006903; DUF618.  
 DR Pfam: PF04618; DUF618; 1.  
 DR SMART: SM00582; RPR; 1.  
 KW Hypothetical protein.  
 SO SEQUENCE 414 AA; 45616 MW; A9C72DBAEC082EC CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 9; DB 10; Length 414;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 34 LAKEEER 42  
 168 LAKEEER 176

RESULT 32  
 ID 09FUP7 PRELIMINARY; PRT; 439 AA.  
 AC 09FUP7:  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Genomic DNA, chromosome 5, p1 clone:MON23 (Hypothetical 48.7 kDa  
 DE protein)  
 DE MON23.12/AT5G65180.  
 GN Arabidopsis thaliana (Mouse-ear cress)  
 OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:Colombia;  
 RA MEDLINE:98403884; PubMed:9734815;  
 RA Kotani H., Nakamura Y., Sato S., Aamizu E., Kaneko T., Miyajima N.,  
 RA Tabata S.,  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.  
 RT Sequence features of the regions of 1,367,185 bp covered by 19  
 RT physically assigned P1 and TAC clones."  
 RL DNA Res. 5:203-216(1998).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Ban J., Chung M.K.,  
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,  
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,  
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Kosemura E.,  
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,  
 RA Palm C.U., Sekurai T., Satou M., Seki M., Shinn P., Southwick A.,  
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.,  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Ban J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,  
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Kim C., Kosemura E., Lam B., Lin J., Meyers M.C., Miranda M.,  
 RA Narusaka M., Nguyen M., Palm C.U., Sekurai T., Satou M., Seki M.,



RA Shin P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RT "Full length cDNA of gene MON23.12/AT5G65180 (GI.10178180).";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB013395; BAB1654.1; -;  
 DR EMBL: AY034943; AAK59449.1; -;  
 DR EMBL: AY063122; AAL34296.1; -;  
 DR InterPro: IPR006903; DUF618.  
 DR InterPro: IPR006569; RPR.  
 DR Pfam: PF04818; DUF618; 1.  
 DR SMART: SM00582; RPR; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 439 AA; 48708 MW; 0058A0EFD9CFC31E CRC64;  
 Query Match 0.6%; Score 9; DB 10; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 9.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 LAKELEEE 42  
 Db 221 LAKELEEE 229  
 RESULT 33  
 O8GUK8 PRELIMINARY; PRT; 469 AA.  
 ID O8GUK8  
 AC O8GUK8  
 DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
 DE Hypothetical protein.  
 GN AT5G10060.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,  
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,  
 RA Deng J.M., Hayashizaki Y., Heuan V.M., Lee J.M., Ishida J., Kamiya A.,  
 RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Shinn P., Tang C.C., Toriumi M., Wong C., Wu H.C.,  
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,  
 RA Davis R.W.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BT002418; AAC00778.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 51954 MW; B1ABA7COFFFF72FB CRC64;  
 Query Match 0.6%; Score 9; DB 10; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 LAKELEEE 42  
 Db 223 LAKELEEE 231  
 RESULT 34  
 O9HY15 PRELIMINARY; PRT; 827 AA.  
 ID O9HY15  
 AC O9HY15  
 DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
 DE Probable transcriptional regulator.  
 GN PA3420.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 NCBI\_TaxID=287;  
 OX

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PAOI;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an  
 opportunistic pathogen.";  
 RL Nature 406:959-964 (2000).  
 CC -1- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL  
 REGULATORS.  
 DR EMBL: AB004763; AAC06808.1; -;  
 DR InterPro: IPR000792; HTH\_LuxR.  
 DR Pfam: PF00196; Gere; 1.  
 DR PRINTS: PR00038; HTHLUXR.  
 DR ProDom: PD000307; HTH\_LuxR; 1.  
 DR SMART: SM00421; HTH\_LuxR; 1.  
 DR PROSITE: PS00622; HTH\_LuxR\_FAMILY; 1.  
 KW DNA-binding; transcription regulation; Complete proteome.  
 SQ SEQUENCE 827 AA; 91779 MW; 69BDB9DA552B41FE CRC64;  
 Query Match 0.6%; Score 9; DB 16; Length 827;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 472 AGSGKTVLL 480  
 Db 42 AGSGKTVLL 50  
 RESULT 35  
 O9ZHW8 PRELIMINARY; PRT; 74 AA.  
 ID O9ZHW8  
 AC O9ZHW8  
 DT 01-MAY-1999 (TEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
 DE Pl 18Bm2.  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE Pl 18Bm2.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M;  
 RX MEDLINE=99003167; PubMed=9784561;  
 RA Godfroid F., Tammlau B., Danese I., Denoel P., Tibor A., Weynants V.,  
 RA Cloeckaert A., Godfroid B., Letesson J.J.;  
 RT "Identification of the permease gene of Brucella  
 melitensis 16M and involvement of lipopolysaccharide O side chain in  
 RT Brucella survival in mice and in macrophages.";  
 RL Infect. Immun. 66:5485-5493 (1998).  
 DR EMBL: AF047478; AAC98619.1; -;  
 DR InterPro: IPR002514; Transposase\_8.  
 DR Pfam: PF01527; Transposase\_8; 1.  
 SQ SEQUENCE 74 AA; 8301 MW; 872D23DB7F2249D8 CRC64;  
 Query Match 0.6%; Score 8; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 59 SEAKRLKT 66  
 Db 37 SEAKRLKT 44  
 RESULT 36  
 O9WUH6 PRELIMINARY; PRT; 111 AA.  
 ID O9WUH6

AC Q9WH6;  
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)  
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
 DE 01-OCT-2002 (T-EMBLrel. 12, Last sequence update)  
 GN Espin (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/c; TISSUE=Testis;  
 RA Bartles J.R., Zheng L., Li A., Wang M.;  
 RT "Organization and chromosomal location of the espin gene in the  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF134857; AAD24481.1; -.  
 FT MBL; MG1:1861630; Espn.  
 FT NON\_TER 1 111  
 SO SEQUENCE 111 AA; 13687 MW; 1243020B580B320 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 11; Length 111;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 158 EEBARLAS 165  
 DB 41 EEBARLAS 48

RESULT 37  
 ID 006500 PRELIMINARY; PRT; 120 AA.  
 AC 006500;  
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DE V-ATPase 2001 (T-EMBLrel. 19, Last annotation update)  
 OS Desulfurococcus sp. (strain SY).  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;  
 OC Desulfurococcaceae; Desulfurococcus.  
 NCBI\_TaxID=59822;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Shibui H., Hamamoto T., Yohda M., Kagawa Y.;  
 RT "The stabilizing residues and the functional domains in the  
 RL hyperthermophilic V-ATPase of Desulfurococcus.";  
 DR Blochem. Biophys. Res. Commun. 0:0-0(1997).  
 FT NON\_TER 1 1  
 SO SEQUENCE 120 AA; 12638 MW; 0BDA732A8C25C1A6 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 1; Length 120;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 ILFGAGLT 110  
 DB 61 ILFGAGLT 68

RESULT 38  
 ID 09YDD1 PRELIMINARY; PRT; 146 AA.  
 AC 09YDD1;  
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)  
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
 DE 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 GN Hypothetical protein APE0982.  
 APE0982.

OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;  
 OC Desulfurococcaceae; Aeropyrum.  
 NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kusuda N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RL Crenarchaeon, Aeropyrum pernix K1.";  
 DR DNA Res. 6:83-101(1999).  
 FT EMBL; AP000060; BAA79966.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 146 AA; 15647 MW; 12F5334D7CBD9D47 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 17; Length 146;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 504 LSLSTRP 511  
 DB 36 LSLSTRP 43

RESULT 39  
 ID 09RSR8 PRELIMINARY; PRT; 147 AA.  
 AC 09RSR8;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 OS Hypothetical protein DR2056.  
 GN DR2056.  
 OC Desulfococcus radiodurans.  
 OC Crenarchaeota; Desulfococcus-Thermus; Deinococci; Deinococcaceae;  
 OC Deinococcaceae; Deinococcus.  
 NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Mofatt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Makarewicz J.J., Lam P., McDonald L., Utechtack T., Zalkow C.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RL radiodurans R1.";  
 DR Science 286:1571-1577(1999).  
 DR EMBL; AA02042; AAF11610.1; -.  
 DR TIGR; DR2056; -.  
 DR InterPro; IPR005184; DUF306.  
 DR Pfam; PF03724; DUF306; 1.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 147 AA; 15874 MW; 73CE41D31BDASCT8 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 16; Length 147;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 888 LOGRTTLT 895  
 DB 109 LOGRTTLT 116

RESULT 40  
 Q8IR03 PRELIMINARY; PRT; 151 AA.  
 AC Q8IR03;  
 DT 01-MAR-2003 (TEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE CG4949-PB.  
 GN CG4949.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abail J.F., Abhyantari A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Bencze P.V., Bertram B.P., Bhandari D., Bolhakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pabloe B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Jaisli M., Houston K.A., Howland T.J., Wei M.H., Ileguam C.,  
 RA Jallil M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murty D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodgerf, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banson J., An H., Baldwin D., Banson J., Beeson K.Y., Busan D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorett V., Doup L.E., Doyle C., Drensek D., Fafan D.,  
 RA Ferrera S., Friese E., Galie R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ileguam C., Jallil M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacle J., Pargag V., Park S., Puri V., Richards B., Scheeler F.,  
 RA Phuanavong S., Pittman G.S., Puri V., Pfeiffer B., Scheeler F.,  
 RA Stapleton M., Strong R., Svitzkas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Mista S., Crosby M.A., Mathews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clump M., Drysdale R., Emmert D., Friese E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Flybase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBD databases.  
 DR EMBL, AE003504; AAN09431.1;  
 SQ SEQUENCE 151 AA; 17120 MW; 8FB66FCBC7026C9A CRC64;  
 Query Match 0.6%; Score 8; DB 5; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1384 SKYTLTQ 1391  
 DB 13 SKYTLTQ 20  
 RESULT 41  
 Q30299 PRELIMINARY; PRT; 152 AA.  
 AC Q30299;  
 DT 01-JAN-1998 (TEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein AF2371.  
 GN AF2371.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirchess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 RA Cotton M.D., Spriggs T., Arlrich P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Gayles S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon Archaeoglobus fulgidus.";  
 RL Nature 390:364-370(1997).  
 DR EMBL, AB001112; AAB91296.1; -  
 DR TIGR, AP2371; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 152 AA; 16646 MW; E16C36C812491BE CRC64;  
 Query Match 0.6%; Score 8; DB 17; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1196 VPFVASLP 1203  
 DB 95 VPFVASLP 102

## RESULT 42

Q9YMI9 PRELIMINARY; PRT; 155 AA.  
 ID Q9YMI9  
 AC Q9YMI9  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE Apoptosis inhibitor  
 OS Lymantoxia inhibitor  
 OC Lymantoxia dispar  
 CC Virusess; dsDNA viruses, no RNA stage; Baculoviridae;  
 NC NCB1\_TaxID=10449;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99124785; PubMed=9887315;  
 RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,  
 RT "Sequence and analysis of the genome of a baculovirus pathogenic for  
 RL Lymantoxia dispar";  
 RN Virology 253:17-34(1999).  
 RP SEQUENCE FROM N.A.  
 RA Kuzio J.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; AF091810; AAC70325.1; -  
 DR HSBP; O13490; 10BH.  
 DR InterPro; IPR001370; BIR.  
 DR Pfam; PF00653; BIR; 1.  
 DR Pfam; PF00653; BIR; 1.  
 DR Pfam; PF00653; BIR; 1.  
 DR SMART; SM00238; BIR; 1.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 1.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 DR Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 155 AA; 17421 MW; A3985F0A84740364 CRC64;  
 Query Match  
 Best Local Similarity 0.6%; Score 8; DB 12; Length 155;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 162 RLASFRNW 169  
 DB 7 RLASFRNW 14

## RESULT 43

Q8ZU27 PRELIMINARY; PRT; 169 AA.  
 ID Q8ZU27  
 AC Q8ZU27  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE Hypothetical protein  
 GN PAE2531.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 NC NCB1\_TaxID=13773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=IM2 / ATCC 51768 / DSM 7523;  
 RA PubMed=11792869;  
 RA Flitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
 RL aerophilum";  
 DR EMBL; AEO09882; AAL64259.1; -  
 DR InterPro; IPR003593; AAA\_Atpase.

DR SMART; SM00382; AAA; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 169 AA; 18439 MW; FEE923FF27669846 CRC64;  
 Query Match  
 Best Local Similarity 0.6%; Score 8; DB 17; Length 169;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 470 GEAGSGKT 477  
 DB 10 GEAGSGKT 17

## RESULT 44

Q9Y329 PRELIMINARY; PRT; 192 AA.  
 ID Q9Y329  
 AC Q9Y329  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE Putative espin (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISUB=Testis;  
 RA Bartles J.R., Zheng L., Li A., Wang M.,  
 RT "Organization and chromosomal location of the espin gene in the  
 RL human";  
 DR EMBL; AF134401; AAD24480.1; -  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 192 AA; 21971 MW; 44236A20760AEEF6 CRC64;  
 Query Match  
 Best Local Similarity 0.6%; Score 8; DB 4; Length 192;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 158 EBRARLAS 165  
 DB 116 EBRARLAS 123

## RESULT 45

Q9VX87 PRELIMINARY; PRT; 197 AA.  
 ID Q9VX87  
 AC Q9VX87  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE CG4949 protein (Drosophila)  
 GN CG4949.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 NC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA Sutcliffe G.C., Mortman J.R., Yandell M.D., Ashburner M., Henderson S.N.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Zhang Q., Chen L.X.,  
 RA Man K.H., Doyle C., Baxter B.G., Heit R.G., Champe M., Pfeiffer B.D.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Baer R.M., Baxter J., Bayraktaroglu L., Beasley B.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ilegem C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissendach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,  
 RA Chape M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,  
 RA Gonzalez M., Gharin H., Li P., Liao G., Miranda A., Mulligan C.J.,  
 RA Nunoo J., Pacled J., Paragas V., Park K., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AEO03504; AAF46691.1; -  
 DR EMBL: AY061506; AAL29054.1; -  
 DR FlyBase: FBgn0030813; CG94949.  
 SQ SEQUENCE 197 AA; 22374 MW; 50BFBD40AD775F6 CRC64;  
 Query Match 0.6%; Score 8; DB 5; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1384 SKYLTILQ 1391  
 Db 59 SKYLTILQ 66  
 RESULT 46  
 P91724 PRELIMINARY; PRT; 202 AA.  
 ID P91724;  
 AC P91724;  
 DT 01-MAY-1997 (TEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)  
 DE NULLO (Fragment).  
 GN NULLO.  
 OS *Drosophila yakuba* (Fruit Fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBT\_TaxID=7245;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IVORY COAST;  
 RX MEDLINE=97051714; PubMed=8896375;  
 RA Caccione A., Moriyama B.N., Gleason J.M., Nigro L., Powell J.R.,  
 RT "A molecular phylogeny for the *Drosophila melanogaster* subgroup and  
 the problem of polymorphism data."

RL Mol. Biol. Evol. 13:1224-1232(1996).  
 DR EMBL: U44732; AAB46423.1; -  
 DR FlyBase: FBgn0020062; Dyak\NULL0.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 202 AA; 22449 MW; F07B62375080307A CRC64;  
 Query Match 0.6%; Score 8; DB 5; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1200 ASLPNPFIS 1207  
 Db 23 ASLPNPFIS 30  
 RESULT 47  
 Q8MVN1 PRELIMINARY; PRT; 213 AA.  
 ID Q8MVN1;  
 AC Q8MVN1;  
 DT 01-OCT-2002 (TEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE Inhibitor of apoptosis protein-like protein.  
 GN IAP.  
 OS *Bolletia villosa*.  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Pyuridae; Bolletia.  
 OC NCBT\_TaxID=63515;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Davidson B.J., Swalla B.J.;  
 RT "A Molecular Analysis of Ascidian Metamorphosis Reveals Activation of  
 an Innate Immune Response."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF483030; AAM76110.1; -  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 1.  
 DR SMART: SM00238; BIR; 1.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 1.  
 SQ SEQUENCE 213 AA; 23948 MW; 4DA34B086971007E CRC64;  
 Query Match 0.6%; Score 8; DB 5; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 216 EHAKEFPK 223  
 Db 108 EHAKEFPK 115  
 RESULT 48  
 Q52735 PRELIMINARY; PRT; 219 AA.  
 ID Q52735;  
 AC Q52735;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
 DE CCMB.  
 GN CCMB.  
 OS *Rhizobium etli*.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 OC NCBT\_TaxID=29449;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CE2;  
 RX MEDLINE=97136701; PubMed=8982078;  
 RA Aguilar G.R., Soberon M.,  
 RT "Cloning and sequence analysis of the *Rhizobium etli* ccma and ccmb  
 genes involved in c-type cytochrome biogenesis."  
 RL Gene 182:129-135(1996).  
 DR EMBL: U52866; AAB40906.1; -

DR InterPro; IPR003544; Cytc\_biog\_Ccmb.  
 DR Pfam; PF03379; Ccmb; 1.  
 DR PRINTS; PR01414; CcmbBIOGNIS.  
 DR TIGRFAMs; TIGR01190; Ccmb; 1.  
 SQ SEQUENCE 219 AA; 22676 MW; 6075082E88AD59C4 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 219;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 LSAALGLD 30  
 58 LSAALGLD 65

RESULT 49  
 ID 08UC11 PRELIMINARY; PRT; 219 AA.  
 AC 08UC11;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DE ABC transporter, membrane spanning protein.  
 GN Ccmb OR ATU2687 OR AGR\_C\_4870.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 RX NCBI\_TaxId=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitzajima J.P.,  
 RA Chou V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,  
 RA Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Boye D., Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutyavin T., Levy R., Li M.-J., McClelland G., Palmer A.,  
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chundley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Neeter E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";  
 RT Science 294:2317-2323(2001).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Houmel K., Goldman B.S., Cao Y., Askenazi M., Halling C., Millin L.,  
 RA Wollan C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,  
 RA Cielo C., Slater S., Gursen J., Lomo C., Sear C., Strub G.,  
 RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";  
 RT Science 294:2323-2328(2001).  
 RL EMBL; AF009215; AAL43668.1;  
 DR EMBL; AF009215; AAL43668.1;  
 DR InterPro; IPR003544; Cytc\_biog\_Ccmb.  
 DR Pfam; PF03379; Ccmb; 1.  
 DR PRINTS; PR01414; CcmbBIOGNIS.  
 DR TIGRFAMs; TIGR01190; Ccmb; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 219 AA; 22807 MW; 8E22F07D055F994D CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 16; Length 219;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 LSAALGLD 30  
 58 LSAALGLD 65

RESULT 50  
 ID 08XFR2 PRELIMINARY; PRT; 230 AA.  
 AC 08XFR2;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DE Putative regulatory protein (putative deor-family transcriptional regulator).  
 GN STM0410 OR STY0448.  
 OS Salmonella typhimurium, and  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 RX NCBI\_TaxId=602, 601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RA MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,  
 RA Ryan B., Sun H., Plorea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";  
 RT Nature 413:852-856(2001).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA SPECIES=S.typhi; STRAIN=CT18;  
 RA MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgensen K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitthead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";  
 RT Nature 413:848-853(2001).  
 RL Nature 413:848-853(2001).  
 DR EMBL; AB008714; AAL19364.1;  
 DR EMBL; AB008714; AAL19364.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 230 AA; 26663 MW; 8809EADFE1EA313B6 CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 16; Length 230;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 468 VEGSAGSG 475  
 51 VEGSAGSG 58

RESULT 51  
 ID 08LB30 PRELIMINARY; PRT; 232 AA.  
 AC 08LB30;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DE DAG protein, putative.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC core eudicots; Brassicales; Brassicaceae; Arabidopsis.  
 RX NCBI\_TaxId=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,

RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RL annotation.";  
RN Genome Biol. 0:0-0(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY087455; AAC65001.1; -; ECBBB44CF961280D CRC64;  
SQ SEQUENCE 232 AA; 26173 MW; ECBBB44CF961280D CRC64;

Query Match 0.6%; Score 8; DB 10; Length 232;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1220 DEBTSEKF 1227  
DB 145 DEBTSEKF 152

RESULT 52  
O9LPZ1 PRELIMINARY; PRT; 232 AA.

AC O9LPZ1;  
DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE T23J18.10 (Hypothetical protein).  
GN ATG11430/T23J18.10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
[1]  
RP SEQUENCE FROM N.A.  
RA Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
RA Kim C., Altafi H., Bel O., Chin C., Chou J., Choi E., Conn L.,  
RA Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Lenz C., Li J., Liu A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,  
RA Toriumi M., Vaysberg M., Yu G., Federpiel N.A., Theologis A.,  
RA Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC T23J18 from chromosome  
RT 1.";  
RN Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RA STRAIN=cv. Columbia;  
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
RA Nakajima M., Enju A., Kamita A., Narusaka M., Carninci P., Kawai J.,  
RA Hayashizaki Y., Shinozaki K.;  
RT "Arabidopsis thaliana full-length cDNA.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC011661; AAF16628.1; -;  
DR EMBL: AK11508; BAC42171.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 232 AA; 26200 MW; 7E26445D058C24EC CRC64;

Query Match 0.6%; Score 8; DB 10; Length 232;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1220 DEBTSEKF 1227  
DB 145 DEBTSEKF 152

RESULT 53  
O9Z2B4 PRELIMINARY; PRT; 253 AA.

AC O9Z2B4;  
DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
DE Small espin.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=Sprague-Dawley; TISSUE=Kidney;  
RX MEDLINE=98437351; PubMed=9763424;  
RA Bartles J.R., Zheng L., Li A., Wierda A., Chen B.;  
RT "Small espin: A third actin-bundling protein and potential forked  
RT protein ortholog in brush border microvilli.";  
RL J. Cell Biol. 143:107-119(1998).  
DR EMBL: AF076856; AAC69563.1; -;  
DR InterPro: IPR003124; WH2.  
DR Pfam: PF02205; WH2; 1.  
DR SMART: SM00246; WH2; 1.  
SQ SEQUENCE 253 AA; 28240 MW; B0C40BB6B605F416 CRC64;

Query Match 0.6%; Score 8; DB 11; Length 253;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 EEBARLAS 165  
DB 178 EEBARLAS 185

RESULT 54  
O9QY27 PRELIMINARY; PRT; 253 AA.

AC O9QY27;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
DE Small espin.  
OS ESN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=129/SvJ;  
RX MEDLINE=20056108; PubMed=10588661;  
RA Chen B., Li A., Wang D., Wang M., Zheng L., Bartles J.R.;  
RT "Espin containing an additional actin-binding site in its N terminus and  
RT is a major actin-bundling protein of the Sertoli cell-spermatid  
RT ectoplasmic specialization junctional plaque.";  
RL Mol. Biol. Cell 10:4327-4339(1999).  
DR EMBL: AF134858; AAF18322.1; -;  
DR MGD: MGI:1861630; Espin.  
DR InterPro: IPR003124; WH2.  
DR Pfam: PF02205; WH2; 1.  
DR SMART: SM00246; WH2; 1.  
SQ SEQUENCE 253 AA; 28086 MW; B0247F7126156916 CRC64;

Query Match 0.6%; Score 8; DB 11; Length 253;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 EEBARLAS 165  
DB 178 EEBARLAS 185

RESULT 55  
O9DD12 PRELIMINARY; PRT; 253 AA.

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AC 09DD12;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN Espn.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Aizawa K., Hara A., Fukushima Y., Konno H., Adachi J., Ishii Y.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kodera K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Plebchmann W., Gaasterland T., Glasi C., King B., Kochava H.,
RA Kueni P., Lewis S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J.,
RA Schimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barn G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Guernich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima T., Mazzarelli U., Mombasets P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyrhew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohenki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RU Nature 409:685-690(2001);
DR EMBL; AF002284; BMB21987.1;
DR MGD; MGI:1861630; Espn.
DR InterPro; IPR003124; WH2.
DR Pfam; PF02205; WH2; 1.
DR SMART; SM00246; WH2; 1.
SQ SEQUENCE 253 AA; 28097 MW; 97A5A133470F487 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 253;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 EEBARLAS 165
DB 178 EEBARLAS 185

RESULT 56
09DGN3
AC 09DGN3; PRELIMINARY; PRT; 268 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Espin (fragment)
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Cochlea;
RX MEDLINE=20427267; PubMed=10975527;
RA Zheng L., Sekerova G., Vranich K., Tlney L.G., Mugnaini E.,
RA Bartles J.R.;
RT "The Deaf Jerker Mouse Has a Mutation in the Gene Encoding the Espin
RT Actin-Bundling Proteins of Hair Cell Stereocilia and Lacks Espins.";
RU Cell 102:377-385(2000).
DR EMBL; AF233885; AAF98133.1;

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DR InterPro; IPR000381; Inhibin_beta.
DR InterPro; IPR002965; P-rich_extens.
DR InterPro; IPR006077; Vinculin/catenin.
DR InterPro; IPR003124; WH2.
DR Pfam; PF02205; WH2; 1.
DR PRINTS; PRO0671; INHIBINB.
DR PRINTS; PRO1217; PRICEXTENS.
DR PRINTS; PRO0806; VINCULIN.
DR SMART; SM00246; WH2; 1.
FT NON TER
SQ SEQUENCE 268 AA; 29103 MW; F815B482B2BB9A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 13; Length 268;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 EEBARLAS 165
DB 192 EEBARLAS 199

RESULT 57
08FLCO
AC 08FLCO; PRELIMINARY; PRT; 307 AA.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Transcriptional activator protein nhar.
GN Nhar OR C0025.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O6:HI / CFT073 / ATCC 700928;
RX MEDLINE=22386234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G., III, Redford P., Roesch P.,
RA Raeko D., Buckles E.L., Lion S.-R., Boutin A., Hacker J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donenberg M.S., Blatner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RU Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016755; AAN78525.1;
KW Complete proteome.
SQ SEQUENCE 307 AA; 34965 MW; 557E680FF7BC14F CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 307;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 NDDSVSEI 1262
DB 259 NDDSVSEI 266

RESULT 58
09X6W1
AC 09X6W1; PRELIMINARY; PRT; 314 AA.
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Class A beta-lactamase precursor TLA-1 (EC 3.5.2.6).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

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RP SEQUENCE FROM N.A.  
RX MEDLINE=20187162; PubMed=10722503;  
RA Silva J., Aguilar C., Ayala G., Estrada M.A., Garza-Ramos U.,  
RA Lara-Iglesias R., Ledezma L.,  
RT "TLA-1: a new plasmid-mediated extended-spectrum beta-lactamase from  
RT Escherichia coli.";  
RL Antimicrob. Agents Chemother. 44:997-1003(2000).  
DR EMBL; AF148067; AAD37403.1; -.  
DR HSSP; P00807; 1BLP.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydroxylase; Plasmid.  
SQ SEQUENCE 314 AA; 34980 MW; 1FB7B53E011D7A53 CRC64;  
  
QY Query Match 0.6%; Score 8; DB 2; Length 314;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 683 ELKATVS 690  
DB 136 ELKATVS 143  
  
RESULT 59  
O98JF7 PRELIMINARY; PRT; 315 AA.  
AC O98JF7;  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical protein ml1963.  
GN ML1963.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idekawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Shimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.,  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AF002998; BAB49209.1; -.  
DR InterPro; IPR001279; Bactamase-like.  
DR Pfam; PF00753; lactamase\_B; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 315 AA; 34032 MW; 7D28710A057035F7 CRC64;  
  
QY Query Match 0.6%; Score 8; DB 16; Length 315;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 297 AALAKGL 304  
DB 72 AALAKGL 79  
  
RESULT 60  
O46012 PRELIMINARY; PRT; 329 AA.  
AC O46012;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ZK228.7 protein.  
GN ZK228.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Basham V.M.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DDBB databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z82086; CAB04998.1; -.  
DR WormBep; ZK228.7; CE16716.  
DR InterPro; IPR003003; TTM\_chemo2.  
DR InterPro; IPR000168; TTM\_nematode.  
DR Pfam; PF01604; Ttm\_5; 1.  
SQ SEQUENCE 329 AA; 36804 MW; F785BAC2AFB24C CRC64;  
  
QY Query Match 0.6%; Score 8; DB 5; Length 329;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1072 LLLTLPST 1079  
DB 249 LLLTLPST 256  
  
RESULT 61  
O8XVS1 PRELIMINARY; PRT; 331 AA.  
AC O8XVS1;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Probable L-arabinose-binding periplasmic (PBP) ABC transporter  
DE protein.  
GN ARAF OR RSC2758 OR R800096.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Ralstoniaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoudat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,  
RA Chaudier M., Choiane N., Claudel-Renard C., Cunha S., Demange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
RA Signier P., Thiebaut P., Whalen M., Wincker P., Levy M.,  
RA Weisenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
RL Nature 415:497-502(2002).  
DR EMBL; AL646071; CAD16465.1; -.  
DR InterPro; IPR001761; Periplasm/Lact.  
DR Pfam; PF00532; Peripla\_BP\_like; 1.  
KW Complete proteome.  
SQ SEQUENCE 331 AA; 35427 MW; 5BFB4064C0F16F8F CRC64;

QY Query Match 0.6%; Score 8; DB 16; Length 331;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 296 VAALAKG 303  
DB 184 VAALAKG 191

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RESULT 62
Q93E95 PRELIMINARY; PRT; 343 AA.
AC Q93E95;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DN D-alamine-D-amine ligase 2.
OS Enterococcus gallinarum.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
ON NCBI_TaxId=1353;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BM4174;
RA Ambur O.H., Reynolds P.E., Arias C.A.;
RT "Characterization of a D-Ala:D-Ala ligase gene flanking the vanC
RT repressor: evidence for the presence of three ligase genes in vancomycin
RT resistant Enterococcus gallinarum."
DR EMBL/AF363615; AAK97387.1; EMBL/GenBank/DBJ databases.
DR InterPro; IPR000291; Data_19_van.
KW Pfam; PF01820; Data_19_van.
SQ SEQUENCE 343 AA; 38454 MW; 4B0E928BF15742F CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 343;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 423 DISSLAT 430
DB 260 DISSLAT 267

RESULT 63
Q57896 PRELIMINARY; PRT; 345 AA.
AC Q57896;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN 345AA long hypothetical transport-ATP binding protein.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
ON NCBI_TaxId=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kouguchi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohtsuka Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Ioshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Maenuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RN DNA Rec. 5:55-76(1998).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
DR EMBL/AP000001; BA029226.1;
DR HSP; Q58663; 166H;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran.
DR Pfam; PF03459; TOBE; 1.
DR ProDom; PD000066; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.

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DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Transport; Complete proteome.
SQ SEQUENCE 345 AA; 38927 MW; 98BB76ADB874C1BF CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 17; Length 345;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 473 GSGKTVLL 480
DB 36 GSGKTVLL 43

RESULT 64
Q8LB55 PRELIMINARY; PRT; 358 AA.
AC Q8LB55;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN Putative aldolase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
ON NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.U., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RN Genome Biol. 0:0-0(2002).
RP SEQUENCE FROM N.A.
RA Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RN EMBL; AY087414; AAM64963.1;
SQ SEQUENCE 358 AA; 38345 MW; 4B30B2AF060D421B CRC64;
Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 358;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 LKSLRG 152
DB 80 LKSLRG 87

RESULT 65
Q82487 PRELIMINARY; PRT; 358 AA.
AC Q82487;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DN T1H20.10 protein (Putative aldolase).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
ON NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RA WASHU;
RT "The A. thaliana Genome Sequencing Project."
RN Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Columbia;
RA Cotton M., Graves T., Sutterer C., Modde T.;
RT "The sequence of A. thaliana t12H20."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Meyers H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamuya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Arabidopsis thaliana full-length cDNA."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF080119; AAC35519.1; -
DR EMBL: AL161516; CAB81176.1; -
DR EMBL: AK18216; BAC42838.1; -
DR HSSP: P23522; IDX.
DR InterPro: IPR005000; HpcH HpaI.
DR Pfam: PF03328; HpcH HpaI; 1.
SQ SEQUENCE 358 AA; 38404 MW; E932B2AF060ECFAD CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 358;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 LKSLRNG 152
DB 80 LKSLRNG 87

RESULT 66
O97H79 PRELIMINARY; PRT; 365 AA.
AC O97H79;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Predicted GTPase, YPAF B. subtilis ortholog.
GN CAC2134.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]_TaxID=1488;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1466286;
RA Neidling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum."
RL EMBL: AE007714; AAK80092.1; -
DR InterPro: IPR004396; Cons_hypoth92.
DR InterPro: IPR006073; GTP_OBG.
DR InterPro: IPR006169; GTP_OBG_sub.
DR Pfam: PF01018; GTP_OBG; 1.
DR PRINTS; PR00326; GTP_OBG.

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DR TIGRPFAM; TIGR00092; TIGR00092; 1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40607 MW; 13CD1F39C2E8D24D CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 365;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 LEEBROKE 45
DB 249 LEEBROKE 256

RESULT 67
O92NG8 PRELIMINARY; PRT; 372 AA.
AC O92NG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative ABC transporter ATP-binding protein.
GN R02237 OR SMC01625.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Batut J.,
RA Boisset P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S.,
RA Gohrie T., Goffeau A., Kahn D., Kiss B., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsberger U.,
RA Renard C., Thebaud P., Vandembol M., Weidner S., Gallibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591790; CAC46816.1; -
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 39835 MW; 6DF9BF0C39C3502C CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 372;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 473 GSGKTVLL 480
DB 39 GSGKTVLL 46

RESULT 68
O8DTQ0 PRELIMINARY; PRT; 372 AA.
AC O8DTQ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN SMU.1280C.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]_TaxID=1309;
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

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RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 RA Li S., Zhu H., Najar P., Lai H., White J., Roe B.A., Perrett J.U.,  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 RT pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).  
 DR EMBL; AE014963; AAN58960.1; -;  
 KW Hypothetical protein, complete proteome.  
 SQ SEQUENCE 372 AA; 42793 MW; 76D427D8B0B511ED CRC64;

Query Match 0.6%; Score 8; DB 16; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 SNEERIL 1242  
 DB 137 SNEERIL 144

RESULT 69  
 Q98DC3 PRELIMINARY; PRT; 390 AA.  
 AC Q98DC3; 01-OCT-2001 (TReMBLrel. 18, Created)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 GN MLI4766.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 RX NCBI\_TaxID=381;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsumoto A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimizu S., Sugimoto M.,  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003004; BAB51348.1; -;  
 DR InterPro; IPR006680; Amidohydro\_1.  
 DR InterPro; IPR003764; Naga.  
 DR Pfam; PF01979; Amidohydro\_1; 1.  
 DR ProDom; PD001248; Naga; 1.  
 DR TrEMBL; TIGR00221; naga; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 390 AA; 40090 MW; AC312A11F1A9F688 CRC64;

Query Match 0.6%; Score 8; DB 16; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 VAAIAKAG 303  
 DB 183 VAAIAKAG 190

RESULT 70  
 Q54143 PRELIMINARY; PRT; 391 AA.  
 AC Q54143; 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 GN Agy1-COA dehydrogenase Redw.  
 DR RBDW OR SC05879 OR SC259.20.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
 OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.

OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Oliver K., Harris D.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Parthill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=1200953;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
 RA Harper D., Bauman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parthill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2).";  
 RL Nature 411:141-147(2002).  
 DR EMBL; AL939125; CAN16488.1; -;  
 DR HSSP; 006319; IBOC.  
 DR InterPro; IPR006090; Agy1-COA dh C.  
 DR InterPro; IPR006091; Agy1-COA dh M.  
 DR InterPro; IPR006092; Agy1-COA dh N.  
 DR Pfam; PF00441; Agy1-COA dh; 1.  
 DR Pfam; PF02770; Agy1-COA dh; 1.  
 DR Pfam; PF02771; Agy1-COA dh; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 391 AA; 41624 MW; 95E01740EC1EB755 CRC64;

Query Match 0.6%; Score 8; DB 16; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LGIDAVOL 34  
 DB 334 LGIDAVOL 341

RESULT 71  
 Q04151 PRELIMINARY; PRT; 396 AA.  
 AC Q04151; 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 GN Rhodopy protein precursor.  
 OS Rhodospirillum rubrum.  
 GN Toxoplasma gondii.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma.  
 RX NCBI\_TaxID=5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH;  
 RX MEDLINE=92178277; PubMed=1542304;

RA Oseorio P.N., Schwartzman J.D., Boothroyd J.C.;  
 RT "A Toxoplasma gondii rhoptry protein associated with host cell  
 RL Mol. Biochem. Parasitol. 50:1-15(1992).  
 DR EMBL; M71274; AAA69859.1; -.  
 DR InterPro; IPR002965; P-rich\_extensn.  
 DR PRINTS; PRO1217; PRICHEXTENSN.  
 KM Signal.  
 FT CHAIN 1 21 POTENTIAL.  
 FT SIGNAL 22 396 RHOPTRY PROTEIN  
 SQ SEQUENCE 396 AA; 42670 MW; 929A1B12540E89E7 CRC64;  
 Query Match 0.6%; Score 8; DB 5; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 105 FGAGLTRL 112  
 DB 363 FGAGLTRL 370  
 RESULT 72  
 Q8JHV9 PRELIMINARY; PRT; 401 AA.  
 AC Q8JHV9;  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 23, Last annotation update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE IAP-like protein.  
 GN ILX.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NC NCB1\_TaxID=8355;  
 OX NCB1\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22038366; PubMed=12021770;  
 RA Holley C.L., Olson M.R., Colon-Ramos D.A., Kornbluth S.;  
 RT "Reaper eliminates IAP proteins through stimulated IAP degradation and  
 RT generalized transcriptional inhibition."  
 RL Nat. Cell Biol. 4:439-444(2002).  
 DR EMBL; AF468029; AAM88215.1; -.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 2.  
 DR SMART; SM00238; BIR; 2.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 2.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 SQ SEQUENCE 401 AA; 45286 MW; F8FDD31AFBFD146 CRC64;  
 Query Match 0.6%; Score 8; DB 13; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 195 VQCFSCGG 202  
 DB 76 VQCFSCGG 83  
 RESULT 73  
 Q9V1Q6 PRELIMINARY; PRT; 422 AA.  
 AC Q9V1Q6;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Hypothetical protein PAB0247.  
 GN PAB0247.  
 OS Pyrococcus abyssi.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.  
 OX NCB1\_TaxID=29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GES / Otsay;  
 RA Heilig R.;  
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
 RT structure and evolution."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ248284; CAB49293.1; -.  
 DR InterPro; IPR004365; tRNA\_anti.  
 DR Pfam; PF01336; tRNA\_anti\_1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 422 AA; 48560 MW; 518B6DA0E810D978 CRC64;  
 Query Match 0.6%; Score 8; DB 17; Length 422;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1353 LPRILRLN 1360  
 DB 38 LPRILRLN 45  
 RESULT 74  
 Q98CE6 PRELIMINARY; PRT; 429 AA.  
 AC Q98CE6;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE Nicotinamide nucleotide transhydrogenase, subunit alpha1.  
 GN MUR5181.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 NC NCB1\_TaxID=381;  
 OX NCB1\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=MAFF303097;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; APO03005; BAB51675.1; -.  
 DR InterPro; IPR004002; Aladh\_PNT.  
 DR Pfam; PF01262; Aladh\_PNT; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 429 AA; 44262 MW; 805F2C6ACF393406 CRC64;  
 Query Match 0.6%; Score 8; DB 16; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 296 VAALAKAG 303  
 DB 104 VAALAKAG 111  
 RESULT 75  
 Q98C91 PRELIMINARY; PRT; 437 AA.  
 AC Q98C91;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Ekopolysaccharide production protein, ExoO.  
 GN MUR5249.

OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003006; BAB51730.1;  
 DR InterPro; IPR007016; Wzy\_C.  
 DR Pfam; PF04932; Wzy\_C; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 437 AA; 48542 MW; 33BBBACD861CFC3C CRC64;

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 16; Length 437;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 891 RTTLTGAL 898  
 |||||  
 Db 112 RTTLTGAL 119

Search completed: December 18, 2003, 09:15:01  
 Job time : 84 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 ; Search time 22 Seconds  
(Without alignments)  
2999.021 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403

Sequence: 1 MATQKASDERISQFDHNL.....SKYLTIQKWLFPSP10K 1403

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1403	100.0	1403	1	BIR1_HUMAN
2	35	2.5	1447	1	BIRB_MOUSE
3	24	1.7	1402	1	BIRG_MOUSE
4	24	1.7	1403	1	BIRA_MOUSE
5	24	1.7	1403	1	BIRE_MOUSE
6	24	1.7	1403	1	BIRF_MOUSE
7	8	0.6	156	1	NUSB_MYCTU
8	8	0.6	179	1	OPLA_HUMAN
9	8	0.6	272	1	DNRI_STRPE
10	8	0.6	290	1	YAS7_METVA
11	8	0.6	324	1	FABH_RHOCA
12	8	0.6	335	1	SPPA_BACSU
13	8	0.6	382	1	KCCI_METAN
14	8	0.6	421	1	SAHH_PYRFU
15	8	0.6	421	1	SAHH_PYRHO
16	8	0.6	489	1	GSPA_ECOLI
17	8	0.6	496	1	BIR4_ECOLI
18	8	0.6	496	1	BIR4_MOUSE
19	8	0.6	548	1	AMDS_EMENT
20	8	0.6	1338	1	ACIN_MOUSE
21	8	0.6	1341	1	ACIN_HUMAN
22	8	0.6	1449	1	DPO3_CLOPE
23	8	0.5	90	1	VAS4_VACCV
24	8	0.5	98	1	YS15_BOBEU
25	8	0.5	106	1	Y266_RICPR
26	8	0.5	117	1	TLB2_MOUSE
27	8	0.5	121	1	YPL4_ARATH
28	8	0.5	134	1	YHCB_ECOLI
29	8	0.5	155	1	IL2_CAPRI
30	8	0.5	175	1	YB43_MYCEN
31	8	0.5	178	1	DSBB_PASMU
32	8	0.5	181	1	HP28_HUMAN
33	8	0.5	184	1	MPL_MPLV

34	7	0.5	196	1	T2D9_DROME	P49306 drosophila
35	7	0.5	207	1	PSMB_PYRAB	Q9v0n9 pyrococcus
36	7	0.5	224	1	DCIL_LYCES	Q42463 lycopersico
37	7	0.5	230	1	DAG_ANTMA	Q38732 antirrhinum
38	7	0.5	231	1	ARAD_BACHD	Q9kbq4 bacillus ha
39	7	0.5	232	1	SMY_MOUSE	P13675 mus musculu
40	7	0.5	232	1	SPIN_HUMAN	Q99865 homo sapien
41	7	0.5	237	1	SPIN_HUMAN	Q9y657 homo sapien
42	7	0.5	239	1	CAUD_MELGA	P13505 melagris g
43	7	0.5	240	1	SPIN_MOUSE	Q61142 mus musculu
44	7	0.5	258	1	CODY_CLOPE	Q8xj95 clostridium
45	7	0.5	258	1	SPN2_HUMAN	Q9b222 homo sapien
46	7	0.5	259	1	MOB2_YEAST	P43653 saccharomyc
47	7	0.5	260	1	CCG6_HUMAN	Q9bxt2 homo sapien
48	7	0.5	260	1	CCG6_MOUSE	Q8vhw3 mus musculu
49	7	0.5	260	1	CCG6_RAT	Q8vhw7 rattus norv
50	7	0.5	261	1	CODY_STRMU	P53388 streptococc
51	7	0.5	269	1	AROE_NEIMU	P95389 neisseria m
52	7	0.5	281	1	YOAC_LACLA	Q9c4b9 lactococcus
53	7	0.5	284	1	MRP_CLOPE	P53381 clostridium
54	7	0.5	286	1	ZAP1_NPVAC	P41435 autographa
55	7	0.5	289	1	ZN75_HUMAN	P51815 homo sapien
56	7	0.5	292	1	METP_BUCAP	Q8x622 buchnera ap
57	7	0.5	295	1	RPSC_MYXXA	Q07083 myxococcus
58	7	0.5	295	1	Y326_MYCGE	P47568 mycoplasma
59	7	0.5	296	1	NIFD_NOSCO	P52337 nostoc comm
60	7	0.5	298	1	BIR7_HUMAN	Q96cas homo sapien
61	7	0.5	300	1	GLXB_RHIME	Q87390 rhizobium m
62	7	0.5	304	1	HEMK_MYCTU	Q10602 mycobacteri
63	7	0.5	308	1	BEH1_SFVI	P29169 simian foam
64	7	0.5	308	1	CITR_BACSU	P39127 bacillus su
65	7	0.5	315	1	GLSA_RHIME	Q92b0 rhicobium m
66	7	0.5	323	1	RPQ4_YEAST	P40339 saccharomyc
67	7	0.5	329	1	DAPF_LISKO	Q8y5n9 listeria mo
68	7	0.5	330	1	XDHA_BACSU	Q32147 bacillus su
69	7	0.5	337	1	YB21_YEAST	P38278 saccharomyc
70	7	0.5	337	1	YO42_CLOPE	Q8xmp0 clostridium
71	7	0.5	350	1	TGDS_HUMAN	Q95455 homo sapien
72	7	0.5	350	1	UXUA_CLOPE	Q8x015 clostridium
73	7	0.5	352	1	HIS8_STRAM	Q99vp9 staphylococ
74	7	0.5	352	1	HIS8_STRAM	Q8xyn3 staphylococ
75	7	0.5	355	1	TGDS_MOUSE	Q8vdr7 mus musculu
76	7	0.5	355	1	Y124_AQUAE	Q67685 aquifex aeo
77	7	0.5	358	1	PIAP_PIG	Q62640 sus scrofa
78	7	0.5	363	1	DP3B_AQUAE	Q67325 aquifex aeo
79	7	0.5	363	1	MODC_RHOCA	Q08381 rhodobacter
80	7	0.5	363	1	MURG_LISIN	Q929y2 listeria in
81	7	0.5	363	1	MURG_LISMO	Q8y5m2 listeria mo
82	7	0.5	363	1	YK12_CABEL	P42169 caenorhabdi
83	7	0.5	364	1	ARRA_DROME	P15372 drosophila
84	7	0.5	366	1	VP09_BRAPS	Q911c5 bacteriopho
85	7	0.5	372	1	TAU2_STRCO	Q9xaco streptococ
86	7	0.5	375	1	GLK1_TRIVA	Q99t29 trichomonas
87	7	0.5	376	1	MPK2_ARATH	Q39022 arabidopsis
88	7	0.5	378	1	FENI_MOUSE	P39749 mus musculu
89	7	0.5	378	1	YN91_ANASP	P46680 anabaena sp
90	7	0.5	380	1	TH11_THETN	Q8r3f0 thermoaer
91	7	0.5	404	1	TH11_BACHD	Q9x804 bacillus ha
92	7	0.5	408	1	PGK_THEAC	Q9h195 thermoplas
93	7	0.5	411	1	PKB3_YEAST	P38911 saccharomyc
94	7	0.5	416	1	PROA_VIBVO	Q8df94 vibrio vuln
95	7	0.5	417	1	YAT1_SYNP6	Q9b447 synechococ
96	7	0.5	423	1	CESS_HUMAN	Q9b477 homo sapien
97	7	0.5	427	1	SY5_CHITE	Q8x866 chlorobium
98	7	0.5	430	1	PURA_STRPN	Q971c1 streptococ
99	7	0.5	438	1	SURA_BUCAL	P57240 buchnera ap
100	7	0.5	432	1	MURD_FUSNN	Q8rdq1 fusobacteri

## ALIGNMENTS

RESULT 1

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EMBL; U19251; AAC52045.1; -  
EMBL; U80017; AAC52047.1; -  
EMBL; U21913; AAA64504.1; -  
EMBL; AC005031; AAC62261.1; -  
HSSP; Q13490; LOBH.  
Genew; HGNC:7634; BIRCL.  
MIM: 600355.  
DR GO: GO:0008169; F:apoptosis inhibitor activity; TAS.  
DR GO: GO:0006916; P:anti-apoptosis; TAS.  
DR GO: GO:0007399; P:neurogenesis; TAS.  
DR InterPro: IPR003593; AAA\_Atpase.  
DR InterPro: IPR001370; BIR\_REPEAT.  
DR InterPro: IPR007111; NACHT\_NTPase.  
DR Pfam; PF00653; BIR\_3.  
DR SMART; SM00382; BIR\_1.  
DR SMART; SM00218; BIR\_3.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS50837; NACHT\_1.  
KM Apoptosis; Repeatc.  
FT REPEAT 60 127 BIR 1.  
FT REPEAT 159 227 BIR 2.  
FT REPEAT 278 345 BIR 3.  
FT DOMAIN 464 758 NACHT.  
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FT CONFLICT 386 387 M -> V (IN REF. 3).  
FT CONFLICT 535 535 Y -> H (IN REF. 3).  
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Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MATOOKASDERISQFDHNLPELSALIGDAVOLAELEEEOKERAMQGVNSOMRE 60  
QY 61 AKRLKFTVTEPYEPPSSWIPQEMAAAGGYFTGVSGIQGFCSSLLFGAGTRLPEDHKRF 120  
DB 61 AKRLKFTVTEPYEPPSSWIPQEMAAAGGYFTGVSGIQGFCSSLLFGAGTRLPEDHKRF 120  
QY 121 HPDGGFLINDVGNIAKVDIRVONLKSRLGKGRVYEEERARLASFRNPFYVGISPCV 180  
DB 121 HPDGGFLINDVGNIAKVDIRVONLKSRLGKGRVYEEERARLASFRNPFYVGISPCV 180  
QY 181 LSAGAGVFTFGKODIVQCFSCGCGGANNBEQDDPKHEAKMPFCEELRSKSSSEITGYI 240  
DB 181 LSAGAGVFTFGKODIVQCFSCGCGGANNBEQDDPKHEAKMPFCEELRSKSSSEITGYI 240  
QY 241 GSYKGFVDITGSHFVNSVQRELPMASATYNDISIFAYPELRDLSFQMDPRESAVGVALA 300  
DB 241 GSYKGFVDITGSHFVNSVQRELPMASATYNDISIFAYPELRDLSFQMDPRESAVGVALA 300  
QY 301 KAGLFYTGIDIVQCFSCGCGCLEKMOEGDDPLDHTRCFPCNCPFLQNKSSAEVTPDLOS 360  
DB 301 KAGLFYTGIDIVQCFSCGCGCLEKMOEGDDPLDHTRCFPCNCPFLQNKSSAEVTPDLOS 360  
QY 361 RGEICELLETTSSNLEDSIAVGPIVPEMAGGEOMQOANLNEOLRAAYTSASFRHMS 420  
DB 361 RGEICELLETTSSNLEDSIAVGPIVPEMAGGEOMQOANLNEOLRAAYTSASFRHMS 420  
QY 421 LDISSDLATDHLICCDLSIASKHSKVPQDEVLPEVFNGLNSVWCVGGEAGSGATVL 480  
DB 421 LDISSDLATDHLICCDLSIASKHSKVPQDEVLPEVFNGLNSVWCVGGEAGSGATVL 480



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Db 481 KKAFLAMAGCCCLARFQVLVFLVLSSTRPDEGLAIIICDQLLEKXGVTXCMENIIQ 540
Qy 541 QLNQVLFLLDDYKEICISIPQVIGKLIQKHLSTRCLLAVNRNRADIRRYLETLEIK 600
Db 541 QLNQVLFLLDDYKEICISIPQVIGKLIQKHLSTRCLLAVNRNRADIRRYLETLEIK 600
Qy 601 APPFYTVCLIRLFSHNMTRLRKFMVYFGKNSLOKIOKTPFVVAICAMHFOYFDPDS 660
Db 601 APPFYTVCLIRLFSHNMTRLRKFMVYFGKNSLOKIOKTPFVVAICAMHFOYFDPDS 660
Qy 661 PDDVAFKSYMERLSLRNKATAEILKATVSSCGELALKGFSCCFEFDNDILAAGVDED 720
Db 661 PDDVAFKSYMERLSLRNKATAEILKATVSSCGELALKGFSCCFEFDNDILAAGVDED 720
Qy 721 EDLTMLCLMSFTQRLRPFRRFISPAFOELACMRLLIHLDSROHODLGLYHLKQINS 780
Db 721 EDLTMLCLMSFTQRLRPFRRFISPAFOELACMRLLIHLDSROHODLGLYHLKQINS 780
Qy 781 PMMTVAANNFLNVSSLPSTKAGPKIVSHLLHVDNKESELENISENDVYLKHQPRISLO 840
Db 781 PMMTVAANNFLNVSSLPSTKAGPKIVSHLLHVDNKESELENISENDVYLKHQPRISLO 840
Qy 841 MQLLRGLWQICPQAYFSMVSEHLVLALKTAYOSNTVAACSPVLOPLQGRITLTGALNL 900
Db 841 MQLLRGLWQICPQAYFSMVSEHLVLALKTAYOSNTVAACSPVLOPLQGRITLTGALNL 900
Qy 901 QYFFDHPESLSLRSHHPFRGNKTSBRAHFSVLETCFDSQVPTIDODYASAFEPNNEM 960
Db 901 QYFFDHPESLSLRSHHPFRGNKTSBRAHFSVLETCFDSQVPTIDODYASAFEPNNEM 960
Qy 961 ERLAKEDNVKSYMORRASPDLSTGYWKLSPKQVKIPCLVDVNDIDVQODMLEIL 1020
Db 961 ERLAKEDNVKSYMORRASPDLSTGYWKLSPKQVKIPCLVDVNDIDVQODMLEIL 1020
Qy 1021 MTFVFSASQRIELHNSRGFIESIRPALBLSKASVTKCSISKLELSAABEHLITLPSLE 1080
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Qy 1081 SLEVSQGTGSGODIPNLDFLCLKLSVDLEGNINVSFVYPEEPNFHMEKLLIOISA 1140
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Qy 1141 EYDPSKLVKLIQNSPNLHVFHLKCNFSDRGSIMTMVSCKLTETIKFSFQOAPFVA 1200
Db 1141 EYDPSKLVKLIQNSPNLHVFHLKCNFSDRGSIMTMVSCKLTETIKFSFQOAPFVA 1200
Qy 1201 SLNPFISLKLINLEGOQFPDEETSEKFAVILGSLSNLEELILPTGDIYVAVAKLIIOCCQ 1260
Db 1201 SLNPFISLKLINLEGOQFPDEETSEKFAVILGSLSNLEELILPTGDIYVAVAKLIIOCCQ 1260
Qy 1261 QHLCLRLVLSFKTLNDSVVEIAKVAISGGPQKLENIKLSINHKITBEGYRNFQALDNM 1320
Db 1261 QHLCLRLVLSFKTLNDSVVEIAKVAISGGPQKLENIKLSINHKITBEGYRNFQALDNM 1320
Qy 1321 PNLQELDISHFECTKAAQATYVKSLSQCLRLPRLIRLMLSMULDADADIALNWKER 1380
Db 1321 PNLQELDISHFECTKAAQATYVKSLSQCLRLPRLIRLMLSMULDADADIALNWKER 1380
Qy 1381 HPOSXYTLIQKWLIPSPPIIOK 1403
Db 1381 HPOSXYTLIQKWLIPSPPIIOK 1403

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RESULT 2
BIRB_MOUSE
ID BIRB_MOUSE STANDARD: PRT; 1447 AA.
AC Q9QUK4; Q9R030;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bsculoviral IAP repeat-containing protein 1b (Neuronal apoptosis
inhibitory protein 2).

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GN BIRCB OR NAIP2 OR NAIP-RS6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Gowney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315342; PubMed=10384056;
RA Varaghi Z., Diez E., Gros P., Mackenzie A.;
RT "cDNA cloning and the 5' genomic organization of Naip2, a candidate
gene for murine Legionella resistance."
RL Mamm. Genome 10:761-763 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=99417674; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunzel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgn1/SMA
interval."
RL Genomics 60:137-151 (1999).
RN [4]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN=129/Sv;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Priesella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgn1 critical interval and contains multiple copies of Naip
exon 5."
RL Genomics 38:405-417 (1996).
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -!- SIMILARITY: Contains 3 BIR repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF135489; AAD56761.1; -
CC EMBL; AF135490; AAD56762.1; -
CC EMBL; AF102871; AAC73002.1; -
CC EMBL; AF131205; AAD56759.1; -
CC EMBL; U66329; AAC52977.1; -
CC PIR; T42628; T42628.
CC HSSP; Q13490; IQBH.
CC MGD; MGI:1298226; Birc1b.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001370; BIR_
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00382; AAA; 1.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.
CC PROSITE; PS01282; BIR_REPEAT_2; 3.
CC PROSITE; PS00837; NACHT; 1.
CC Apoptosis; Repeat; Multigene family.
CC REPEAT 60 127 BIR 1.
CC REPEAT 159 227 BIR 2.
CC REPEAT 278 345 BIR 3.
CC DOMAIN 508 802 NACHT.

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FT CONFLICT 377 377 D -> G (IN REF. 3).
FT CONFLICT 403 403 L -> F (IN REF. 3).
FT CONFLICT 478 478 L -> I (IN REF. 3).
FT CONFLICT 540 540 N -> Y (IN REF. 3).
FT CONFLICT 862 862 K -> N (IN REF. 3).
FT CONFLICT 1079 1080 SD -> FN (IN REF. 3).
FT CONFLICT 1089 1089 R -> C (IN REF. 3).
FT CONFLICT 1115 1115 K -> E (IN REF. 3).
FT CONFLICT 1122 1122 T -> A (IN REF. 3).
FT CONFLICT 1136 1136 D -> E (IN REF. 3).
FT CONFLICT 1157 1157 S -> G (IN REF. 3).
FT CONFLICT 1167 1167 S -> R (IN REF. 3).
FT CONFLICT 1271 1271 F -> C (IN REF. 3).
SQ SEQUENCE 1447 AA, 164033 MW, 98F6C6A73BA60A2 CRC64,

Query Match
Best Local Similarity 2.5%; Score 35; DB 1; Length 1447;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 193 DTVOCFSCGCGCAGNMEGDDPWKEHAKWPKCEFL 227
Db 193 DTVOCFSCGCGCAGNMEGDDPWKEHAKWPKCEFL 227

RESULT 3
BIRG_MOUSE STANDARD; PRT; 1402 AA.
AC Q9JIB3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
GN inhibitory protein 7).
GN BIRCI1 OR NAIP1 OR NAIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 NACHT domain.
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CC or send an email to license@lsb-sib.ch).
CC EMBL; AF242433; AAF82749.1; -
CC HSSP; Q13490; IOBH.
CC MGD; MGI:1858256; Birc1g.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 2.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS0837; NACHT; 1.
CC Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 2.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1402 AA, 159662 MW, C1DFBNA3598931E0D CRC64,

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Query Match
Best Local Similarity 1.7%; Score 24; DB 1; Length 1402;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 204 LGNMEGDDPWKEHAKWPKCEFL 227
Db 204 LGNMEGDDPWKEHAKWPKCEFL 227

RESULT 4
BIRG_MOUSE STANDARD; PRT; 1403 AA.
AC Q9QWK5; Q9JIB5; Q9R017;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1a (Neuronal apoptosis
GN inhibitory protein 1).
GN BIRCI1 OR NAIP1 OR NAIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Varaghi Z., Korneluk R.G., Mackenzie A.E.;
RA "Cloning and characterization of the multiple copies of the murine
RT homologue of NAIP (neuronal apoptosis inhibitory protein).";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431676; PubMed=10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts".
RL Mamm. Genome 10:1032-1035(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414747; PubMed=10958627;
RA Endrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
RT "Genomic sequence analysis of the mouse Naip gene array.";
RL Genome Res. 10:1095-1102(2000).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 NACHT domain.
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CC EMBL; AF007769; AAB69223.1; -
CC EMBL; AF135491; AAD56763.1; -
CC EMBL; AF242432; AAF82752.1; -
CC HSSP; Q13490; IOBH.
CC MGD; MGI:1298223; Birc1a.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001370; BIR.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00653; BIR; 3.
CC SMART; SM00382; AAA; 1.
CC SMART; SM00238; BIR; 3.
CC PROSITE; PS01282; BIR_REPEAT_1; 1.
CC PROSITE; PS0143; BIR_REPEAT_2; 3.
CC PROSITE; PS0837; NACHT; 1.
CC Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.

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CC REPEAT 278 345 BIR 3.
FT DOMAIN 464 758 NACHT.
FT CONFLICT 343 343 I -> V (IN REF. 2).
FT CONFLICT 359 359 L -> Q (IN REF. 2).
FT CONFLICT 624 624 E -> K (IN REF. 2).
FT CONFLICT 1092 1092 D -> E (IN REF. 3).
FT CONFLICT 1116 1116 G -> N (IN REF. 3).
FT CONFLICT 1123 1123 D -> R (IN REF. 3).
FT CONFLICT 1129 1129 L -> H (IN REF. 1).
FT CONFLICT 1140 1140 T -> M (IN REF. 2).
FT CONFLICT 1269 1269 A -> V (IN REF. 3).
SQ SEQUENCE 1403 AA; 158692 MW; B31630259595EE67 CRC64;

Query Match
Best Local Similarity 1.7%; Score 24; DB 1; Length 1403;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNMBEGDDPMKEHAKMPKCEFL 227
Db 204 LGNMBEGDDPMKEHAKMPKCEFL 227

RESULT 5
BIR_MOUSE STANDARD; PRT; 1403 AA.
ID BIR_MOUSE
AC 09J186; 009121; 009122; P81703; Q9R029;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
inhibitory protein 5).
GN BIRCE OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99417674; PubMed=10486205;
RA Endrizzi M., Huang S., Scharf J.M., Growney J.D., Dietrich W.F.;
RA Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Lgnl/SMA
interval."
RT Genomics 60:137-151(1999).
(3)
RN SEQUENCE OF 82-168 FROM N.A.
RP STRAIN=129/Sv;
RC MEDLINE=97131520; PubMed=8975718;
RX Scharf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgnl critical interval and contains multiple copies of Naip
exon 5."
RT Genomics 38:405-417(1996).
(2)
RN FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
SIGNALS.
(1) SIMILARITY: Contains 3 BIR repeats.
(1) SIMILARITY: Contains 1 NACHT domain.
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CC EMBL; AF135492; AAD56764.1; -.
DR EMBL; AF131205; AAD56760.1; -.
DR EMBL; U66326; AAC52974.1; -.
DR HSPF; Q13490; IQBH.
DR MGD; MGI:1298220; Bircle.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR007111; NACHT_NTPase.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00238; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 3.
DR PROSITE; PS50837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
FT CONFLICT 92 92 S -> R (IN REF. 1).
FT CONFLICT 144 144 S -> G (IN REF. 1).
FT CONFLICT 242 242 T -> A (IN REF. 2).
FT CONFLICT 472 472 A -> D (IN REF. 2).
FT CONFLICT 516 516 A -> T (IN REF. 2).
FT CONFLICT 521 521 V -> A (IN REF. 2).
FT CONFLICT 533 533 S -> I (IN REF. 2).
FT CONFLICT 538 538 E -> D (IN REF. 2).
FT CONFLICT 1092 1092 H -> L (IN REF. 2).
FT CONFLICT 1129 1129 R -> Q (IN REF. 2).
FT CONFLICT 1137 1137 V -> I (IN REF. 2).
FT CONFLICT 1242 1242 D -> N (IN REF. 2).
FT CONFLICT 1276 1276
SQ SEQUENCE 1403 AA; 159695 MW; B27F645043BC6C42 CRC64;

Query Match
Best Local Similarity 1.7%; Score 24; DB 1; Length 1403;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 LGNMBEGDDPMKEHAKMPKCEFL 227
Db 204 LGNMBEGDDPMKEHAKMPKCEFL 227

RESULT 6
BIR_MOUSE STANDARD; PRT; 1403 AA.
ID BIR_MOUSE
AC 09J186; 009121; 009122; P81704;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Baculoviral IAP repeat-containing protein 1f (Neuronal apoptosis
inhibitory protein 6).
GN BIRCF OR NAIP6 OR NAIP-RS4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
(1)
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=97131520; PubMed=8975718;
RA Scharf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgnl critical interval and contains multiple copies of Naip
exon 5."
RT Genomics 38:405-417(1996).
(2)
RN SEQUENCE OF 82-168 FROM N.A.
RP STRAIN=129/Sv;
RC MEDLINE=97131520; PubMed=8975718;
RX Scharf J.M., Damron D., Friessella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Lgnl critical interval and contains multiple copies of Naip
exon 5."
RT Genomics 38:405-417(1996).

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CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 NACHT domain.
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CC -----
DR EMBL: AF242431; AAF22751.1;
DR EMBL: U66327; AAC52975.1;
DR HSSP: Q13490; 10BH.
DR MGD: MGI:1298222; B1rc1f.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR007111; NACHT_NTPase.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0837; NACHT; 1.
DR Apoptosis; Repeat; Multigene family.
FT REPEAT 60 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 464 759 NACHT.
SQ SEQUENCE 1403 AA; 159823 MW; 9D4912503358C4E9 CRC64;

Query Match
Best Local Similarity 1.7%; Score 24; DB 1; Length 1403;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 LGNWECDGPWKEHAKFKPCPEL 227
DB 204 LGNWECDGPWKEHAKFKPCPEL 227

RESULT 7
NUB MYCTU STANDARD; PRT; 156 AA.
ID NUB MYCTU
AC P95020; 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE N ubi-2003 (Rel. 42, Last annotation update)
GN N ubi-2003 (Rel. 42, Last annotation update)
OS NUB OR RV2533C OR MT2508 OR MCT159.23.
OC Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
ON NCBI_Taxid=1773;
RX [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin R., Feltwell T., Gentile S., Hamlin N., Holroyd S.,
RA Honanby T., Jags K., Kirogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., O'Boone J., Quail M.A., Rajandream M.A., Rogers R.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulten J.E., Taylor K., Whitehead S., Bartell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[2]
SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Hatt D., Hickey E.,

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RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uitterlind T., Weidman J., Kouri H., Gill J., Mikala A.,
RA Blahut W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RU Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RA MEDLINE=20343008; PubMed=10881194;
RA Gopal B., Haire L.F., Cox R.A., Colston M.J., Major S.,
RA Brannigan J.A., Smerdon S.J., Dodson G.;
RA "The crystal structure of NubA from Mycobacterium tuberculosis."
RL Nat. Struct. Biol. 7:475-478(2000).
CC -1- FUNCTION: INVOLVED IN THE TRANSCRIPTION TERMINATION PROCESS
CC (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: BELONGS TO THE NUB FAMILY.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 144.
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CC -----
DR EMBL: Z83863; CAB06175.1;
DR EMBL: AB007097; AAK64918.1; ALT_FRAME.
DR PIR: A70658; A70658.
DR PDB: 1EYV; 29-NOV-00.
DR TIGR: MT2608;
DR Tuberculin; RV2533C;
DR HAMAP: MF 00073; -; 1.
DR InterPro: IPR006027; NUBB.
DR Pfam: PF01029; NubB; 1.
KW Transcription termination; RNA-binding; 3D-structure;
KW Complete proteome.
FT HELIX 10 27
FT TURN 28 28
FT HELIX 31 44
FT TURN 46 47
FT HELIX 53 64
FT TURN 65 65
FT HELIX 66 74
FT TURN 75 76
FT TURN 78 79
FT HELIX 82 84
FT TURN 87 102
FT TURN 104 105
FT HELIX 108 122
FT TURN 125 126
FT HELIX 127 138
SQ SEQUENCE 156 AA; 16740 MW; 84923E642CA5FD15 CRC64;

Query Match
Best Local Similarity 0.6%; Score 8; DB 1; Length 156;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 AVQLAKEL 38
DB 115 AVQLAKEL 122

RESULT 8
OPLA HUMAN STANDARD; PRT; 179 AA.
ID OPLA HUMAN
AC O14841;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-oxoprolinase (EC 3.5.2.9) (5-oxo-L-prolinease) (Pyroglutamatease)

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DE (5-OPase) (Fragment).
GN OPLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Debella L.R., Wood S.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE CLEAVAGE OF 5-OXO-L-PROLINE TO FORM L-
CC GLUTAMATE COUPLED TO THE HYDROLYSIS OF ATP TO ADP AND INORGANIC
CC PHOSPHATE.
CC -1- CATALYTIC ACTIVITY: ATP + 5-oxo-L-proline + 2 H(2)O = ADP +
CC phosphate + L-glutamate.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
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CC -----
CC EMBL: AF024673; AAB81519.1; -.
CC EMBL: AF024672; AAB81519.1; JOINED.
CC DR GENEW; HGNC:8149; OPLAH.
CC DR MIM; 260005; -.
CC DR InterPro: IPR003692; Hydantoinease_B.
CC DR Pfam: PF02538; Hydantoinease_B; 1.
CC KM Hydrolyase.
CC FT NON_TER 1 1
CC FT NON_TER 179 179
CC SQ SEQUENCE 179 AA; 19334 MW; BA13A42PECABE8EE CRC64;

Query Match 0.6%; Score 8; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 PEVFGNLTN 463
DB 101 PEVFGNLTN 108

RESULT 9
DNR1 STRPE STANDARD; PRT; 272 AA.
AC P25047;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Regulatory protein dnrl.
GN DNR1.
OS Streptomyces puceatus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 29050;
RA MEDLINE=92104954; PubMed=1729206;
RA Stutzman-Engwall K.J.; Otten S.L.; Hutchinson C.R.;
RT "Regulation of secondary metabolism in Streptomyces spp. and
RT overproduction of daunorubicin in Streptomyces puceatus.";
RL J. Bacteriol. 174:144-154(1992).
CC -1- FUNCTION: MAY FORM, WITH DNRJ A TWO-COMPONENT REGULATORY SYSTEM
CC FOR DAUNORUBICIN BIOSYNTHESIS GENES.
CC -1- SIMILARITY: BELONGS TO THE AFSR/DNRJ/REDD FAMILY OF REGULATORS.
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CC -----
CC EMBL: M80237; AAA26736.1; -.
CC DR PIR; A43306; A43306.
CC DR InterPro: IPR005158; BAD.
CC DR InterPro: IPR001867; Trans_reg_C.
CC DR Pfam; PF03704; BTAD; 1.
CC DR Pfam; PF00486; trans_reg_C; 1.
CC DR ProDom; PD000329; Trans_reg_C; 1.
CC KM Antibiotic biosynthesis; Transcription regulation; DNA-binding.
CC SQ SEQUENCE 272 AA; 29698 MW; 97B59E1175030D93 CRC64;

Query Match 0.6%; Score 8; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSAL 26
DB 185 LPELSAL 192

RESULT 10
YAS7 METUA STANDARD; PRT; 290 AA.
ID YAS7 METUA
AC Q58457;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative glycosyl transferase MJ1057 (EC 2.---.-).
GN MJ1057.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.W., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U67549; AAB99061.1; -.
CC DR HSSP; P39621; IQCQ.
CC DR TIGR; MJ1057; -.
CC DR InterPro: IPR001173; Glyco_trans_2.
CC DR Pfam; PF00535; Glycosyltransferase; Complete proteome.
CC KM Hypothetical protein; Transferase; Complete proteome.
CC SQ SEQUENCE 290 AA; 35099 MW; 3F6A1B21C420D74 CRC64;

Query Match 0.6%; Score 8; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 12;

```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1366 LDADDIAL 1373  
 Db 97 LDADDIAL 104

RESULT 11  
 FASH\_RHOCA  
 ID FASH\_RHOCA STANDARD; PRT; 324 AA.  
 AC P30790;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 3-oxoacyl-(acyl-carrier-protein) synthase III (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase III) (KAS III).  
 GN FASH.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 OX NCBI\_TaxId=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9207365; PubMed=1961742;  
 RA Toussein B., Bosc C., Richard P., Colbeau A., Vignais P.M.;  
 RT "A mutation in a Rhodospirillum rubrum gene encoding an integration host factor-like protein impairs in vivo hydroxymethylase expression.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10749-10753 (1991).  
 CC -1- FUNCTION: CATALYZES THE CONDENSATION REACTION OF FATTY ACID FROM MALONYL-ACP. KAS III CATALYZES THE FIRST CONDENSATION REACTION WHICH INITIATES FATTY ACID SYNTHESIS AND MAY THEREFORE PLAY A ROLE IN GOVERNING THE TOTAL RATE OF FATTY ACID PRODUCTION. POSSESSES BOTH ACETOACETYL-ACP SYNTHASE AND ACETYL TRANSACYLASE ACTIVITIES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: acyl-[acyl-carrier protein] + malonyl-(acyl-carrier protein) = 3-oxoacyl-(acyl-carrier protein) + CO(2) + [acyl-carrier protein].  
 CC -1- PATHWAY: Fatty acid biosynthesis.  
 CC -1- SIMILARITY: BELONGS TO THE FASH FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M84030; AAA26127.1; -  
 CC PIR; C41608; C41608.  
 CC DR HSP; P24249; 1HNK.  
 CC DR InterPro; IPR004655; Fash.  
 CC DR TIGRFAMs; TIGR00747; fash.1.  
 CC KM Pacyl acid biosynthesis; Transferase; Acyltransferase;  
 CC KM Multifunctional enzyme.  
 CC FT ACT SITE 114 114 BY SIMILARITY.  
 CC FT ACT SITE 251 251 BY SIMILARITY.  
 CC FT ACT SITE 281 281 BY SIMILARITY.  
 CC SQ SEQUENCE 324 AA; 33732 MW; 7303B987655A20E CRC64;  
 Query Match 0.64; Score 8; DB 1; Length 324;  
 Beel Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 297 ALAKAGL 304  
 Db 233 ALAKAGL 240

AC 034525;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative signal peptide peptidase sppa (EC 3.4.21.-).  
 GN SPPA.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxId=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunz F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertorello M.G., Bessieres P., Borchert S.,  
 RA Borriello R., Boudreau N., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Eutian K.D., Errington J., Fabret C., Ferrari B., Foulger D.,  
 RA Filtz C., Glaeser P., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Giallardi G., Guy B.U., Haga K., Halech J., Harwood C.R., Hanaut A.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones U.,  
 RA Joris B., Karamata D., Kasahara Y., Klaere-Blanchard N., Klein C.,  
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapides A., Lardinois S., Lauber U., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Malet C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynold S.,  
 RA Plescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynold S.,  
 RA Rieger T., Scanlan E., Schleich S., Roche E., Roche B., Sadale Y.,  
 RA Sato T., Scanlan E., Schleich S., Roche E., Roche B., Sadale Y.,  
 RA Sekiguchi J., Sekowka E., Serror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takemaru K., Takemaru K., Takemaru K., Takemaru K., Takemaru K.,  
 RA Takemaru K., Takemaru K., Takemaru K., Takemaru K., Takemaru K.,  
 RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vasserolet A.,  
 RA Viari A., Wandut R., Wedler H., Weitzneger T., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Yata K.,  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."  
 RT Nature 390:249-256 (1997).  
 RL [3]  
 RN [3]  
 RP FUNCTION.  
 RX STRAIN=168;  
 RX MEDLINE=99386931; PubMed=10455123;  
 RA Bolhuis A., Matzen A., Hyyrylaenen H.-L., Kontinen V.P., Meima R.,  
 RA Chapuis J., Venema A., Bron S., Frendl R., van Dijk J.M.,  
 RA "Signal peptide peptidase- and ClpP-like proteins of Bacillus subtilis required for efficient translocation and processing of secretory proteins."  
 RT J. Biol. Chem. 274:24585-24592 (1999).  
 CC -1- FUNCTION: DIGESTION OF THE CLEAVED SIGNAL PEPTIDES (BY SIMILARITY). REQUIRED FOR EFFICIENT PROCESSING OF PRECURSORS UNDER CONDITIONS OF HYPER-SECRETION.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.  
 CC -----  
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CC -----

DR EMBL; AF008220; AAC00312.1; -

DR EMBL; Z99119; CAB14931.1; -

DR PIR; E69990; E69990.

DR MEROPS; S49.001; -

DR Subtilisin; BG13839; sppA.

DR InterPro; IPR002142; Peptidase U7.

DR InterPro; IPR004635; SigPase SppA36.

DR Pfam; PF01343; Peptidase U7; 1.

DR ProDom; PD002887; Peptidase U7; 1.

DR TIGRPFAM; TIGR00706; SppA\_dom; 1.

KW Hydrolyase; Protease; Transmembrane; Complete proteome.

FT TRANSMEM 6 POTENTIAL.

SQ SEQUENCE 335 AA; 36673 MW; 10BDA2DE857D28B CRC64;

Query Match 0.6%; Score 8; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1082 LEVSGTQ 1089  
DB 63 LEVSGTQ 70

RESULT 13

ID KCCL\_METAN STANDARD; PRT; 382 AA.

AC 014408;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE 15-JUL-1998 (Rel. 36, Last annotation update)

OS Calcium/calmodulin-dependent protein kinase (EC 2.7.1.123).

OC Metathiazium antioxiplae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;

OC Microsporid Clavicipitaceae; Metarhizium.

NCBI\_TaxID=5530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M61 / ARSEP 2575;

RA Joshi L., St. Leger R.J., Bldochka M.J., Roberts D.W.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DBD databases.

CC -1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -----

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CC -----

DR EMBL; U28358; AAB80685.1; -

DR HSSP; Q63450; 1A06.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002290; Ser Thr\_kinase.

DR Pfam; PF00069; kinase; 1.

DR ProDom; PD000001; Prot kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR Transferrase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding.

KW Phosphorylation; ATP-binding.

FT DOMAIN 23 278 PROTEIN KINASE.

FT NP\_BIND 29 37 ATP (BY SIMILARITY).

FT BINDING 50 50 ATP (BY SIMILARITY).

FT ACT SITE 142 142 BY SIMILARITY.

FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).

SQ SEQUENCE 382 AA; 43532 MW; 9DA32959F4CA35E0 CRC64;

Query Match 0.6%; Score 8; DB 1; Length 382;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 DHNLLPEL 23  
DB 285 DHNLLPEL 292

RESULT 14

ID SAHH\_PYRFU STANDARD; PRT; 421 AA.

AC P50251;

DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase).

GN AHCY OR PF0343.

OS Pyrococcus furiosus.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

NCBI\_TaxID=2261;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

RL The complete sequence of the Pyrococcus furiosus genome.;

RT Submitted (FEB-2002) to the EMBL/GenBank/DBD databases.

RN [2]

RP SEQUENCE OF 1-169 FROM N.A.

RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;

RA MEDLIN=95184006; PubMed=7878465;

RA Chan M.K.S., Mukund S., Kletzin A., Adams M.W.W., Rees D.C.;

RT "Structure of a hyperthermophilic tungstopterin enzyme, aldehyde ferredoxin oxidoreductase.;"

RL Science 267:1463-1469 (1995).

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine + L-homocysteine.

CC -1- COFACTOR: NAD (By similarity).

CC -1- PATHWAY: Activated methyl cycle.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.

CC -----

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CC -----

DR EMBL; AE010158; AL080467.1; -

DR EMBL; X79777; CA56173.1; -

DR HSSP; P10760; 1B3R.

DR HAMAP; MF\_00563; -; 1.

DR InterPro; IPR000043; Ado\_hcyase.

DR Pfam; PF05221; AdoHcyase; 1.

DR Pfam; PF00670; AdoHcyase NAD; 1.

DR TIGRPFAM; TIGR00936; ahcY; 1.

DR PROSITE; PS00738; ADOHCYASE\_1; 1.

DR PROSITE; PS00739; ADOHCYASE\_2; 1.

KW Hydrolyase; NAD; One-carbon metabolism; Complete proteome.

FT NP\_BIND 211 242 NAD (POTENTIAL).

SQ SEQUENCE 421 AA; 47383 MW; 4ED68F631CBA12B CRC64;

Query Match 0.6%; Score 8; DB 1; Length 421;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VAALAKAG 303  
DB 296 VAALAKAG 303

Db 89 VAAALAKAG 96

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RESULT 15
SAHH_PYRHO STANDARD; PRT; 421 AA.
AC Q56275;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adenosylhomocysteinease (EC 3.3.1.1) (S-adenosyl-L-homocysteine
hydrolyase) [Adocycase].
GN AHCV OR PH0540
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=9834437; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hasegawa A., Negai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Fuchisashi T., Tanaka T., Kudoh Y., Yamazaki Y., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Rep. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenosine
+ L-homocysteine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
-----
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-----
DR EMBL: AP000002; BAA29629.1; ALT_INIT.
DR HAMAP: P10760; 1B3R.
DR HSSP: P10760; 1B3R.
DR InterPro: IPR000043; Adc_hcvase.
DR Pfam: PF05221; Adocycase; 1.
DR Pfam: PF0670; Adocycase; 1.
DR TIGRFAMs: TIGR00936; ahcv; 1.
DR PROSITE: PS00738; ADHCYASE_1; 1.
DR PROSITE: PS00739; ADHCYASE_2; 1.
DR K01: K01; Adocycase; 1.
DR NP BIND: 211 242 NAD (POTENTIAL)
SQ SEQUENCE 421 AA; 47273 MW; 5BE8049F5E5D951E CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 VAAALAKAG 96

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RESULT 16
GSPA_ECOLI STANDARD; PRT; 489 AA.
AC P45756;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable general secretion pathway protein A.
GN GSPA OR B3323
OS Bacteriella coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Zhao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE EXPA FAMILY.
-----
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-----
DR EMBL: U18997; AA58120.1; -.
DR EMBL: AE000409; AAC76348.1; -.
DR F1R; F65125; F65125.
DR Ecogene; EG12888; GSPA.
RT Transport; ATP-binding; Complete proteome.
FW NP BIND 26
SQ SEQUENCE 489 AA; 55298 MW; 7C7DB238274E15C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 GEAGSGKT 33

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RESULT 17
B1R4_MOUSE STANDARD; PRT; 496 AA.
AC Q60989; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacterial IAP repeat-containing protein 4 (inhibitor of apoptosis
protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN B1R4 OR API3 OR XIAP OR AIPA OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Pule K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
[2]
RP SEQUENCE FROM N.A.
RA Parahani R., Lefebvre C., Korneluk R.G., Mackenzie A.B.;

```



RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9  
 CC (By similarity).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
 CC inhibit apoptotic suppressor activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3  
 CC and -7, while the third BIR is involved in caspase-9 inhibition.  
 CC The interactions with SMAC and PRSS25 are mediated by the second  
 CC and third BIR domains (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: Contains 3 BIR repeats.  
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -----  
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 CC -----  
 CC EMBL: U36842; AAC2594.1; -;  
 CC EMBL: U88990; AAB58376.1; -;  
 CC HSSP: Q13490; IOBH.  
 CC MGD: MGI:107572; Birc4.  
 CC InterPro: IPR001370; BIR.  
 CC InterPro: IPR001841; Znf\_ring.  
 CC Pfam: PF00653; BIR; 3.  
 CC SMART: SM00238; BIR; 3.  
 CC SMART: SM00184; RING; 1.  
 CC PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 CC PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 CC PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC PROSITE: PS50089; ZF\_RING\_2; 1.  
 CC Apoptosis; Zinc-finger; Repeat.  
 CC BIR 1.  
 CC REPEAT 26 93 BIR 2.  
 CC REPEAT 163 230 BIR 3.  
 CC REPEAT 264 329 BIR 3.  
 CC ZN\_RING 449 484 RING-TYPE.  
 CC FT CONFLECT 208 208 E -> K (IN REF. 2).  
 CC FT CONFLECT 317 317 E -> D (IN REF. 2).  
 CC FT CONFLECT 317 317 W -> C (IN REF. 2).  
 CC FT CONFLECT 322 322 S -> P (IN REF. 2).  
 CC FT CONFLECT 346 346 S -> P (IN REF. 2).  
 CC FT CONFLECT 360 360 S -> P (IN REF. 2).  
 CC FT CONFLECT 388 388 I -> L (IN REF. 2).  
 CC FT CONFLECT 449 449 C -> S (IN REF. 2).  
 CC FT CONFLECT 462 462 V -> F (IN REF. 2).  
 CC FT CONFLECT 468 468 V -> A (IN REF. 2).  
 CC FT CONFLECT 490 490 K -> N (IN REF. 2).  
 CC SEQUENCE 496 AA; 56079 MW; EC5FPAE0799F2CDD8 CRC64;  
 SO  
 Query Match 0.6%; Score 8; DB 1; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 193 DTVOCFSC 200  
 DB 59 DTVOCFSC 66  
 RESULT 18  
 BIR4\_RAT  
 ID BIR4\_RAT STANDARD; PRT; 496 AA.  
 AC Q9R016;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis  
 DE protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)  
 DE (IAP homolog A) (RIAP3) (RIAP-3).  
 GN BIRC4 OR API3 OR XIAP.  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Saito N.;  
 RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap) mRNA";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9  
 CC (By similarity).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
 CC inhibit apoptotic suppressor activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- DOMAIN: The second BIR domain is sufficient to inhibit caspase-3  
 CC and -7, while the third BIR is involved in caspase-9 inhibition.  
 CC The interactions with SMAC and PRSS25 are mediated by the second  
 CC and third BIR domains (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.  
 CC -1- SIMILARITY: Contains 3 BIR repeats.  
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -----  
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 CC -----  
 CC EMBL: AB033366; BAA85304.1; -;  
 CC HSSP: Q13490; IOBH.  
 CC InterPro: IPR001370; BIR.  
 CC InterPro: IPR001841; Znf\_ring.  
 CC Pfam: PF00653; BIR; 3.  
 CC SMART: SM00238; BIR; 3.  
 CC SMART: SM00184; RING; 1.  
 CC PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
 CC PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 CC PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC PROSITE: PS50089; ZF\_RING\_2; 1.  
 CC Apoptosis; Zinc-finger; Repeat.  
 CC BIR 1.  
 CC REPEAT 26 93 BIR 2.  
 CC REPEAT 163 230 BIR 3.  
 CC REPEAT 264 329 BIR 3.  
 CC ZN\_RING 449 484 RING-TYPE.  
 CC FT CONFLECT 208 208 E -> K (IN REF. 2).  
 CC FT CONFLECT 317 317 E -> D (IN REF. 2).  
 CC FT CONFLECT 317 317 W -> C (IN REF. 2).  
 CC FT CONFLECT 322 322 S -> P (IN REF. 2).  
 CC FT CONFLECT 346 346 S -> P (IN REF. 2).  
 CC FT CONFLECT 360 360 S -> P (IN REF. 2).  
 CC FT CONFLECT 388 388 I -> L (IN REF. 2).  
 CC FT CONFLECT 449 449 C -> S (IN REF. 2).  
 CC FT CONFLECT 462 462 V -> F (IN REF. 2).  
 CC FT CONFLECT 468 468 V -> A (IN REF. 2).  
 CC FT CONFLECT 490 490 K -> N (IN REF. 2).  
 CC SEQUENCE 496 AA; 56072 MW; E250B3C77461A469 CRC64;  
 SO  
 Query Match 0.6%; Score 8; DB 1; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 193 DTVOCFSC 200  
 DB 59 DTVOCFSC 66  
 RESULT 19  
 AMLS\_EMENT  
 ID AMLS\_EMENT STANDARD; PRT; 548 AA.  
 AC P08158;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DE Acetamidase (EC 3.5.1.4).  
 DE AMLS.  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OX NCBI\_TaxID=162425;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87248110; PubMed=3036667;  
 RA Corrick C.M., Twomey A.P., Hynes M.J.;

RT "The nucleotide sequence of the amds gene of *Aspergillus nidulans* and  
 RL the molecular characterization of 5' mutations";  
 CC Gene 53:63-71(1987).  
 CC -1- FUNCTION: Allows acetamide to be used as a sole carbon or  
 CC nitrogen source.  
 CC -1- CATALYTIC ACTIVITY: A monocarboxylic acid amide + H(2)O = a  
 CC monocarboxylate + NH(3).  
 CC -1- INDUCTION: ACETATE INDUCTION MEDIATED BY FACB REGULATORY GENE AND  
 CC PROBABLY BY AMDA REGULATORY GENE. OMEGA AMINO ACID INDUCTION IS  
 CC DEPENDENT ON AMDR REGULATORY GENE.  
 CC -1- SIMILARITY: BELONGS TO THE AMIDASE FAMILY.  
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 CC -----  
 DR EMBL: M16371; AAA33295.1; -  
 DR PIR: A26511; A26511.  
 DR InterPro: IPR000120; Amidase.  
 DR Pfam: PF01425; Amidase; 1.  
 DR PROSITE: PS00571; AMIDASES; 1.  
 DR KMW HydroLase.  
 SQ SEQUENCE 548 AA; 60228 MW; 1EC6368CB867C630 CRC64;  
 Query Match Best Local Similarity 100.0%; DB 1; Length 548;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 296 VAALAKAG 303  
 Db 343 VAALAKAG 350  
 RESULT 20  
 ACIN\_MOUSE STANDARD; PRT; 1338 AA.  
 ID ACIN\_MOUSE  
 AC Q9J1X8; Q9CSN7; Q9CSR9; Q9CSX7; Q9R046; Q9R047;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Apoptotic chromatin condensation inducer in the nucleus (Acinus).  
 GN ACINUS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOPFORMS 2 AND 3).  
 RX MEDLINE=99418558; PubMed=10490026;  
 RA Sahara S., Aceto M., Eguchi Y., Imamoto N., Yoneda Y., Teujimoto Y.,  
 RT "Acinus is a caspase-3-activated protein required for apoptotic  
 RL chromatin condensation.";  
 RN Nature 401:168-173(1999).  
 RN (2)  
 RP SEQUENCE FROM N.A. (ISOPFORM 1).  
 RX Mamoru A., Satsuko S., Yoshitake T.,  
 RT "Molecular cloning of murine acinus, a gene for apoptotic chromatin  
 RL condensation.";  
 RN Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-1190 FROM N.A. (ISOPFORMS 1, 2 AND 4).  
 RX STRAIN=C57BL/6J; TISSUE=Embryo and Pancreas;  
 RA MEDLINE=23354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nishida I., Otsu N., Saito R., Suzuki H., Yamahara I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojohori T.,  
 RA Baldirelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schurml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaestlerland T., Gariboldi M., Giesl C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Marchionni L., McKenna L., Miki H.,  
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Peres G., Pesole G.,  
 RA Petrovsky N., Piliat R., Pontus J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed P.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner B., Wanless C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boriss A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,  
 RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Itoh Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs.";  
 CC Nature 420:563-573(2002).  
 CC -1- FUNCTION: Induces apoptotic chromatin condensation after  
 CC activation by CASP3 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=L;  
 CC IsoId=Q9J1X8-1; Sequence=Displayed;  
 CC Name=2; Synonyms=S;  
 CC IsoId=Q9J1X8-2; Sequence=VSP\_004030, VSP\_004033;  
 CC Name=3; Synonyms=S';  
 CC IsoId=Q9J1X8-3; Sequence=VSP\_004031;  
 CC Name=4;  
 CC IsoId=Q9J1X8-4; Sequence=VSP\_004032;  
 CC -1- PTM: Undergoes proteolytic cleavage; the processed form is active,  
 CC contrary to the uncleaved form (By similarity).  
 CC -1- SIMILARITY: Contains 1 SAP domain.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
 CC in position 110 and 112.  
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 CC -----  
 DR EMBL: AF124725; AAD56723.1; -  
 DR EMBL: AF124729; AAD56727.1; -  
 DR EMBL: AF168782; AAF89661.1; ALT\_FRAMB.  
 DR EMBL: AK011598; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AK012099; BAB28030.1; -  
 DR EMBL: AK012337; BAB28171.2; -  
 DR EMBL: AK050467; BAC34272.1; ALT\_INIT.  
 DR MGD; MGI:1891824; Acinus.  
 DR GO; GO:0005730; C:nucleolus; IDA.  
 DR InterPro: IPR000504; RNA\_rec\_mot.  
 DR InterPro: IPR003034; SAP.  
 DR Pfam: PF02037; SAP; 1.  
 DR SMART; SM00513; SAP; 1.  
 DR PROSITE; PS50800; SAP; 1.  
 KW Apoptosis; Nuclear protein; Alternative splicing.  
 FT DOMAIN 72 106  
 FT DOMAIN 142 443  
 FT DOMAIN 569 667  
 FT DOMAIN 1113 1130  
 FT DOMAIN 1131 1338  
 FT SITE 1093 1094  
 FT VARSPLIC 1 757  
 /FTId=VSP\_004030.  
 /FTId=VSP\_004030. (BY SIMILARITY).  
 Missing (in isoform 2).

```

FT  VARSPLIC 1 773 Missing (in isoform 3).
FT  VARSPLIC 164 204 /FTId=VSP_004031.
FT  VARSPLIC 164 204 EASAESEDEHTHEGVALPDPFGSLNRPETLSTHSBR
FT  VARSPLIC 758 766 -> G (in isoform 4).
FT  VARSPLIC 758 766 /FTId=VSP_004032.
FT  VARSPLIC 758 766 ESRRHTTV-> MFSDSRAG (in isoform 2).
FT  VARSPLIC 758 766 /FTId=VSP_004033.
FT  VARSPLIC 244 244 T-> A (IN REF. 2).
FT  VARSPLIC 515 515 T-> A (IN REF. 2).
FT  VARSPLIC 515 515 F-> L (IN REF. 2).
FT  VARSPLIC 536 536 G-> D (IN REF. 2).
FT  VARSPLIC 557 557 H-> Y (IN REF. 2).
FT  VARSPLIC 568 568 V-> A (IN REF. 2).
FT  VARSPLIC 599 599 S-> I (IN REF. 2).
FT  VARSPLIC 729 729 L-> P (IN REF. 2).
FT  VARSPLIC 757 757 T-> A (IN REF. 1; AAD56723).
FT  VARSPLIC 773 773 MISSING (IN REF. 3; BAB28030).
FT  VARSPLIC 829 829 Q-> R (IN REF. 3; BAB28030).
FT  VARSPLIC 896 896 G-> R (IN REF. 3; BAB28030).
FT  VARSPLIC 1035 1035
SQ  SEQUENCE 1338 AA; 150690 MW; B912D9CB5750FBFA CRC64;

Query Match 0.6%; Score 8; DB 1; Length 1338;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEBOKER 46
DB 1255 EEEBOKER 1262

RESULT 21
ACIN HUMAN STANDARD; PRT: 1341 AA.
ID ACIN HUMAN
AC Q9UKV3; Q75158; Q9UG91; Q9UKV1; Q9UKV2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptotic chromatin condensation inducer in the nucleus (Acinus).
GN ACINUS OR KIA0670.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCB1 Taxid=9606;
OX [1]
RN RP AND MUTAGENESIS OF ASP-1093.
RP MEDLINE=9418558; PubMed=10490026;
RX Sahara S., Aoto M., Eguchi Y., Imamoto N., Yoneda Y., Tsujimoto Y.;
RA "Acinus is a caspase-3-activated protein required for apoptotic
RT chromatin condensation."
RL Nature 401:168-173(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=Uterus;
RA Wambutt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Fetal brain;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL "Full-length cDNA libraries and normalization."
RN Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 56-1341 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=98403880; PubMed=9734811;
RX Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RL DNA Res. 5:169-176(1998).
CC -1- FUNCTION: Induces apoptotic chromatin condensation after

```

```

CC activation by CASP3.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=L;
CC IsoId=Q9UKV3-1; Sequence=Displayed;
CC Name=2; Synonyms=S';
CC IsoId=Q9UKV3-2; Sequence=VSP_004025, VSP_004028;
CC Name=3; Synonyms=S;
CC IsoId=Q9UKV3-3; Sequence=VSP_004026, VSP_004029;
CC Name=4;
CC IsoId=Q9UKV3-4; Sequence=VSP_004027;
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- PTM: Undergoes proteolytic cleavage; the processed form is active,
CC contrary to the uncleaved form.
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF124726; AAD56724.1; -
DR EMBL; AF124727; AAD56725.1; -
DR EMBL; AF124728; AAD56726.1; -
DR EMBL; AL050382; CAB43681.1; -
DR EMBL; BX247975; CAB62309.1; -
DR EMBL; AB014570; BAA31645.2; -
DR Genew; HGNC:17066; ACINUS.
DR MIM; 604562; -
DR InterPro; IPR000504; RNA_rec_mot.
DR InterPro; IPR003034; SAP.
DR Pfam; PF02037; SAP; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Apoptosis; Nuclear protein; Alternative splicing.
FT DOMAIN 72 106 SAP.
FT DOMAIN 142 442 GLU-RICH.
FT DOMAIN 573 676 SER-RICH.
FT DOMAIN 1114 1131 PRO-RICH.
FT DOMAIN 1132 1341 ARG/ASP/GLU/LYS-RICH.
FT SITE 1093 1094 CLEAVAGE (BY CASPASE-3).
FT VARSPLIC 1 727 Missing (in isoform 2).
FT VARSPLIC 1 758 Missing (in isoform 2).
FT VARSPLIC 1 1152 Missing (in isoform 3).
FT VARSPLIC 1 1152 /FTId=VSP_004026.
FT VARSPLIC 728 766 Missing (in isoform 4).
FT VARSPLIC 728 766 /FTId=VSP_004027.
FT VARSPLIC 728 766 /FTId=VSP_004028.
FT VARSPLIC 728 766 /FTId=VSP_004029.
FT MUTAGEN 1093 1093 D->A: ABOLISHES CLEAVAGE BY CASP3 AND
FT CONFLICT 139 139 Q-> H (IN REF. 4).
SQ SEQUENCE 1341 AA; 151887 MW; 8FE28661F63AB5C CRC64;

Query Match 0.6%; Score 8; DB 1; Length 1341;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEBOKER 46
DB 1256 EEEBOKER 1263

RESULT 22
DPO3_CLOPE

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ID DPO3_CLOPE STANDARD; PRT; 1449 AA.
AC O8XCR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN POLC OR CPE1691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohnari K., Hiraoka H., Ohsima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA] (N).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE C FAMILY. POLC
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AP003191; BAB8197.1; -.
DR HAMAP; MF 00356; -.
DR InterPro; IPR006054; DnaQ.
DR InterPro; IPR006055; Exonuclease.
DR InterPro; IPR004013; PNP_C.
DR InterPro; IPR003141; PNP_N.
DR InterPro; IPR006308; PolC_gram_pos.
DR Pfam; PF00929; Exonuclease; 1.
DR Pfam; PF02811; PNP_C; 1.
DR Pfam; PF02231; PNP_N; 1.
DR SMART; SM00479; EXOIII; 1.
DR SMART; SM00481; POLIIIAC; 1.
DR TIGRfam; TIGR00573; dnaq; 1.
DR TIGRfam; TIGR01405; polC Gram_pos; 1.
KW Nucleotidylase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Nuclease; Exonuclease; Complete proteome.
FT DOMAIN 435 598 EXONUCLEASE.
SQ SEQUENCE 1449 AA; 163627 MW; AE24E2CE7D372B85 CRC64;
Query Match
Best Local Similarity 0.6%; Score 8; DB 1; Length 1449;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 679 KATAEIK 686
Db 584 KATAEIK 591

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RESULT 23
V454_VACCV STANDARD; PRT; 90 AA.
AC P21072; P24767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 16-OCF-2001 (Rel. 40, Last annotation update)
OG Protein A54.

```

```

GN A54L OR SALFD.
OS Vaccinia virus (strain WR) and
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254, 10249;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91259063; PubMed=2045793;
RA Smith G.L., Chan Y.S., Howard S.T.;
RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RT J. Gen. Virol. 72:1349-1376(1991).
RN [2]
RP SEQUENCE OF 1-81 FROM N.A.
RC STRAIN=WR;
RX MEDLINE=9111982; PubMed=1846491;
RA Howard S.T., Chan Y.S., Smith G.L.;
RT "Vaccinia virus homologues of the Shope fibroma virus inverted
RT terminal repeat proteins and a discontinuous ORF related to the tumor
RT necrosis factor receptor family.";
RL Virol. 180:633-647(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Copenhagen;
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Proletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virol. 179:247-266(1990).
RN [4]
RP COMPLETE GENOME.
RC STRAIN=Copenhagen;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Proletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";
RL Virol. 179:517-563(1990).
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CC -----
DR EMBL; M35027; AAA48187.1; -.
DR EMBL; M58054; -; NOT_ANNOTATED_CDS.
DR FPI; B42523; B42523.
SQ SEQUENCE 90 AA; 10800 MW; F3F9E9CE52D3B608 CRC64;
Query Match
Best Local Similarity 0.5%; Score 7; DB 1; Length 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1269 SFFKTLN 1275
Db 43 SFFKTLN 49

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```

RESULT 24
V515_BORBU STANDARD; PRT; 98 AA.
AC P70841;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCF-2001 (Rel. 40, Last annotation update)
OG Hypothetical lipoprotein BBD15 precursor.
GN BBD15 OR CDSK.
OS Borrelia burgdorferi ( Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

```

```

OX NCB1_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=97086634; PubMed=893323;
RA Barbour A.G., Carter C.J., Bundoc V., Hinnebusch J.;
RT "The nucleotide sequence of a linear plasmid of Borrelia burgdorferi
RT reveals similarities to those of circular plasmids of other
RT prokaryotes.";
RL J. Bacteriol. 178:6635-6639(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty J., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kierlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Ulfersback T., Matthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential). STRONG, TO B. BURGDOFFERI BPF20.
CC -1- SIMILARITY: STRONG, TO B. BURGDOFFERI BPF20.
CC -----
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CC -----
DR EMBL: UA3414; AAB38559.1; -.
DR EMBL: AE000793; AAC66348.1; ALT_INIT.
DR TIGR: BBD15; -.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
DR Pfam: Hypothetical protein; Lipoprotein; Membrane; Signal;
KW Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 98 HYPOTHETICAL LIPOPROTEIN BBD15.
FT LIPID 22 22 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 98 AA; 11513 MW; F5B57A33ACFE41C6 CRC64;

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RX MEDLINE=99039499; PubMed=9823893;
RA Anderson S.G.E., Zomorodipour A., Anderson J.O.,
RA Sicheitiz-Ponten T., Almark U.C.M., Podowski R.M., Neslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0091 FAMILY.
CC -----
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CC -----
DR EMBL: AJ235271; CAI4728.1; -.
DR PIR: F71681; F71681.
DR InterPro: IPR005133; Phag_MnHg_YuFB.
DR Pfam: PF03334; Phag_MnHg_YuFB_1.
DR TIGRfam: TIGR01300; CPA3_mnHg_phag; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 106 AA; 11775 MW; FD7DB12887F165BF CRC64;

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Query Match 0.5%; Score 7; DB 1; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 477 TVLTKKI 483
Db 98 TVLTKKI 104

```

RESULT 26  
 TLB2 MOUSE STANDARD; PRT; 117 AA.  
 AC P56811;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE TGL1B2 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20056259; PubMed=10588720;  
 RA Hallas C., Pekarsky Y., Itoyama T., Varnum J., Bichi R.,  
 RA Rothstein J.L., Croce C.M.;  
 RT "Genomic analysis of human and mouse TGL1 loci reveals a complex of  
 RT tightly clustered genes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:14418-14423(1999).  
 CC -1- SIMILARITY: BELONGS TO THE TGL1 FAMILY.  
 CC -----
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 CC -----
 DR EMBL: AF195489; AAF12802.1; -.
 DR MGD: MGI:1351609; Tc11b2.
 DR InterPro: IPR004833; TGL1B.
 DR Pfam: PF015575; TGL1B; 1.
 KW Multigene family.
 SQ SEQUENCE 117 AA; 13672 MW; A6B0851165E9B0AA CRC64;

Query Match 0.5%; Score 7; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 57;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 MAAGPY 87  
Db 1 MAAGPY 7

## RESULT 27

YPL4\_ARATH  
ID YPL4\_ARATH STANDARD; PRT; 121 AA.  
AC 09156;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Yippee-like protein At3G5890.  
GN At3G5890 OR F7K19.70.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroidae II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_Taxid=3702;

## SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;  
RX MEDLINE=21016720; PubMed=11130713;  
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unefeld M.,  
FA Farmanoubar B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,  
RA Deleney M., Bourry M., Grivell L.A., Maché R., Pigdomenech P.,  
RA De Simone V., Cholene N., Artiguenave F., Robert C., Brotier P.,  
RA Wincker P., Catolico L., Weissbach J., Saurin W., Queller F.,  
RA Schuster M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wümbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,  
RA Wiedemann R., Kranz H., Voss H., Holland N., Brandt P., Nyakatura G.,  
RA Vezzi A., D'Angelo M., Palavicini A., Toppi S., Simionati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordel G.,  
RA Reichelt J., Scharte M., Schoen O., Barges M., Terol J., Clement J.,  
RA Navarro P., Collado C., Perez-Perez A., Oltenswelder B., Duchemin D.,  
RA Cooke R., Lande M., Berger-Liaou C., Purnelle B., Masny D.,  
RA de Haan M., Maeser A.C., Alcaraz J.-P., Cortet A., Casacuberta E.,  
RA Monfort A., Argilou A., Flores M., Liguori R., Vitale D.,  
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Meyer K.F.X., Kaul S., Town C.D., Koo H.L., Zaccaria P., Mewes H.-W.,  
RA Rooney T., Rizzo M., Walters A., Utecherack T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,  
RA Pal G., Miltschener J., Sellers P., Gill J.B., Feldblyum T.V.,  
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,  
RA Frazer C.M., Kaneo T., Nakamura Y., Sato S., Kato J., Asanizu E.,  
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,  
RA Nakayama S., Kohara M., Matsunoto M., Matsuno A., Muraki A.,  
RA Nakagawa S., Yamada M., Yasuda M., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Takeuchi C., Wada T.,  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
thaliana".  
RL Nature 406:820-822(2000).  
RN [2]

## SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;  
RX Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,  
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
SSP consortium (Salk/Stanford/PBSC)".  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE YIPPEE FAMILY.

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DR EMBL: AL163632; CAB87843.1; -

DR EMBL: AY050951; AAK93628.1; -  
DR EMBL: AY091443; AAM14382.1; -  
DR PIR: T49201; T49201.  
DR InterPro: IPR004910; Yippee.  
DR Pfam: PF03226; Yippee; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 121 AA; 13592 MW; 10B66E2450AB31 CRC64;

## Query Match

Best Local Similarity 0.5%; Score 7; DB 1; Length 121;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1109 VDLGNT 1115  
Db 7 VDLGNT 13

## RESULT 28

YHCB\_ECOLI  
ID YHCB\_ECOLI STANDARD; PRT; 134 AA.  
AC P39435;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein yhcB.  
GN YHCB OR B3233 OR C3987 OR Z4592 OR EGS4106.  
OS Escherichia coli.  
OS Escherichia coli O6, and  
OC Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_Taxid=562, 217992, 83334;  
RN [1]

## SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor U., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.,  
RT "The complete genome sequence of Escherichia coli K-12".  
RL Science 277:1453-1474(1997).  
RN [2]

## SEQUENCE FROM N.A.

RC STRAIN=O6:HI / CPT073 / ATCC 700928;  
RX MEDLINE=22388234; PubMed=12471157;  
RA Welch R.A., Burland V., Plunkett G., III, Redford P., Roesch P.,  
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.,  
RT "Extensive mosaic structure revealed by the complete genome sequence  
of uropathogenic Escherichia coli".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
RN [3]

## SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11206551;  
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor U., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,  
RA Apodaca J., Nantharathan T.S., Iln J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.,  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7".  
RL Nature 409:529-533(2001).  
RN [4]

## SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo H., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
RA Kunara S., Shiba T., Hattori M., Shingawa H.,

```

RT RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RT DNA Ref. 8:11-22(2001).
RN [5]
RN SEQUENCE OF 10-134 FROM N.A.
RC STRAIN=K12 / M3110;
RA Baas S., Gu Q., Goddard A.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO H.INFLUENZAE H11628.
CC -----
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CC -----
DR EMBL; U18997; AAA58035.1; -
DR EMBL; AB000402; AAC76265.1; -
DR EMBL; AE016767; AAN82427.1; -
DR EMBL; AE005551; AAG58361.1; -
DR EMBL; AF002564; BAB37529.1; -
DR EMBL; U15661; -; NOT_ANNOTATED_CDS.
DR PIR; B91142; B91142.
DR PIR; C6515; C6515.
DR PIR; B85987; B85987.
DR Ecogene; EG12614; yncB.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 134 AA; 15239 MW; F357F30A599661B7 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ILPELSA 25
DB 86 ILPELSA 92

RESULT 29
ID IL2_CAPHI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxId=925;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimestad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Beyer J.C., Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-2 family.
CC -----
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CC -----
DR EMBL; X76063; AAA33664.1; -
DR EMBL; U34274; AAB38527.1; -
DR PIR; S38662; S38662.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KM Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20
FT CHAIN 1 155
FT CARBOHYD 23 23
FT DISULFID 79 127
FT CONFLICT 3 5
FT CONFLICT 22 22
FT CONFLICT 30 30
FT CONFLICT 51 51
FT CONFLICT 71 71
FT CONFLICT 89 89
FT CONFLICT 99 99
FT CONFLICT 107 113
FT CONFLICT 140 140
FT CONFLICT 144 144
FT CONFLICT 154 154
SQ SEQUENCE 155 AA; 17703 MW; 90022DFBB6AF78D8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1294 LENTKLS 1300
DB 51 LENTKLS 57

RESULT 30
ID YB43_MYCPN STANDARD; PRT; 175 AA.
AC P75143;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN143 (E07_orf175).
GN MPN143 OR MP011.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxId=2104;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
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CC -----  
 DR EMBL: U41745; AAC50462.1; -  
 DR EMBL: AC004922; AAF03506.1; -  
 DR EMBL: BC000684; AAH00684.1; -  
 DR EMBL: BC007873; AAH07873.1; -  
 DR EMBL: U65960; AAB07135.1; -  
 DR Genew: HGNC:14634; PDAP1.  
 DR MIM: 607075; -  
 DR GO: GO:0008283; P:cell proliferation; TAS.  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 KW Phosphorylation.  
 FT CONFLICT 1 1 M -> MI (IN REF. 4).  
 FT CONFLICT 13 13 R -> W (IN REF. 4).  
 FT CONFLICT 25 25 A -> T (IN REF. 4).  
 FT CONFLICT 29 29 A -> S (IN REF. 4).  
 FT CONFLICT 67 67 E -> D (IN REF. 4).  
 FT CONFLICT 80 80 L -> F (IN REF. 4).  
 FT CONFLICT 126 126 K -> R (IN REF. 4).  
 SO SEQUENCE 181 AA; 20630 MW; P97914C7920ABAB3 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 EEBEOKE 45  
 Db 36 EEBEOKE 42

## RESULT 33

MPL\_MPLV STANDARD; PRT; 184 AA.  
 AC P40931;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Myeloproliferative leukemia protein.  
 GN V-MPL.  
 OS Myeloproliferative leukemia virus (MPLV).  
 OC Viruses; Retroviruses; Retroviridae.  
 OX NCBI\_TaxId=11973;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9108483; PubMed=2175677;  
 RA Souyri M., Vigon I., Pencillet J.-F., Heard J.-M., Tambourin P.,  
 RA Wendling F.;  
 RT "A putative truncated cytokine receptor gene transduced by the  
 RT myeloproliferative leukemia virus immortalizes hematopoietic  
 RT progenitors.";  
 RL Cell 63:1137-1147(1990).  
 CC -1- FUNCTION: TRUNCATED FORM OF THE RECEPTOR FOR THROMBOPOIETIN.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS AN ENV-MPL  
 CC POLYPEPTIDE.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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Query Match 0.5%; Score 7; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 LSALLGL 29  
 Db 56 LSALLGL 62

## RESULT 34

T2D9 DROME STANDARD; PRT; 196 AA.  
 AC P49306; Q9V190;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transcription initiation factor TFIID 28 kDa subunit beta  
 DE (p28-beta) (TAFLI30 beta).  
 GN TAFII OR TAF30-BETA OR CG4079.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94102540; PubMed=8276241;  
 RA Yokomori K., Chen J.-L., Admon A., Zhou S., Tian R.,  
 RT "Molecular cloning and characterization of dTAFII30 alpha and  
 RT dTAFII30 beta: two small subunits of Drosophila TFIID.";  
 RT Gene Dev. 7:2587-2597(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Nakatani Y.;  
 RL Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=2019606; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Plamkosh C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu B., Beasley E.M.,  
 RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.D., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kamali B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milne N.V., Moadary C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Mizny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzone M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun B.,  
 RA Svirides R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Messarman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: TPRIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A  
 CC CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS  
 CC AND REPRESSORS.  
 CC -1- SUBUNIT: TPRIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A  
 CC NUMBER OF TBP-ASSOCIATED FACTORS (TAFs).  
 CC -1- SUBCELLULAR LOCATION: Nucleus.  
 CC -1- SIMILARITY: BELONGS TO THE TAF21 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, S67660; AAB29541.1; -  
 DR EMBL, U06457; AAB19245.1; -  
 DR EMBL, AE003626; AARS2806.1; -  
 DR PIR, B49453; B49453.  
 DR TRANSFAC: T02131;  
 DR FLYBASE: FBgn0011281; Tafi1.  
 DR InterPro: IPR004822; Histone\_core.  
 DR Pfam: PF04719; TAFI128; 1.  
 DR TrnscRpt: TAFI128; 1.  
 FT DOMAIN 80 87 FOLY-GLU.  
 FT SEQUENCE 196 AA; 22091 MW; E8528553F598AC9 CRC64;  
 SQ  
 Query Match 0.5%; Score 7; DB 1; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 KELESEE 42  
 DB 79 KELESEE 85

CC -1- SUBUNIT: COMPOSED OF TWO SUBUNITS, ALPHA AND BETA. THE COMPLEX IS  
 CC FORMED OF FOUR RINGS. THE TWO OUTER RINGS ARE EACH COMPOSED OF  
 CC SEVEN ALPHA SUBUNITS. THE TWO INNER RINGS ARE EACH COMPOSED OF  
 CC SEVEN BETA SUBUNITS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to peptidase family T1B.  
 CC -----  
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 CC -----  
 DR EMBL, AJ248285; CAB49664.1; -  
 DR PIR, G75118; G75118.  
 DR HSSP: P28061; IPMA.  
 DR MEROPS: T01.002; -  
 DR InterPro: IPR000243; Proteasome\_B.  
 DR InterPro: IPR001353; Proteasome.  
 DR Pfam: PF00227; Proteasome; 1.  
 DR PRINTS: PR00141; PROTEASOME.  
 DR PROSITE: PS00854; PROTEASOME\_B; 1.  
 DR Proteasome; Hydrolase; Protease; Complete proteome.  
 FT PROPEP 1 10 APPARENTLY REMOVED IN MATURE FORM (BY  
 FT CHAIN 11 207 PROTEASOME BETA SUBUNIT.  
 FT ACT SITE 11 11 PROBABLY.  
 FT SEQUENCE 207 AA; 22671 MW; 9FBD9B0519434939 CRC64;  
 SQ  
 Query Match 0.5%; Score 7; DB 1; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1305 IITERGYR 1311  
 DB 188 IITERGYR 194

RESULT 36  
 DCL\_LYCERS  
 ID DCL\_LYCERS STANDARD; PRT; 224 AA.  
 AC 042463;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DE DCL protein, chloroplast precursor (Defective chloroplasts and leaves  
 DE protein).  
 GN DCL.  
 OS Lycopersicon esculentum (tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Honeymaker;  
 RX MEDLINE=97015121; PubMed=8861949;  
 RA Keddie J.S., Carroll B., Jones J.D.G., Grussem W.;  
 RT "The DCL gene of tomato is required for chloroplast development and  
 RT palisade cell morphogenesis in leaves.";  
 RL EMBO J. 15:4208-4217(1996).  
 CC -1- FUNCTION: HAS A FUNCTION IN THE EARLY STAGE OF CHLOROPLAST  
 CC DEVELOPMENT AND PALISADE CELL MORPHOGENESIS.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast.  
 CC -----  
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CC -----
DR EMBL; U55278; AAC9434.1; -
DR EMBL; U55219; AAC9433.1; -
DR PIR; S71749; S71749.
KM Chloroplast; Transit peptide.
FT TRANSIT 1 50
FT CHAIN 51 224 DCL PROTEIN.
SQ SEQUENCE 224 AA; 25438 MW; 15703EF39F58179D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 224;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 LETSES 374
Db 74 LETSES 80

RESULT 37
DAG_ANTMA . STANDARD; PRT; 230 AA.
ID DAG_ANTMA . STANDARD; PRT; 230 AA.
AC Q38732;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DAG protein, chloroplast precursor.
GN DAG.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Lamiales; Antirrhinaceae; Antirrhineae;
OC Antirrhinum.
OC NCBI_TaxID=4151;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Leaf;
RX MEDLINE=97015120; PubMed=8861948;
RA Characterize M., Sparvoli S., Edmunds C., Garosi P., Findlay K.,
RA Martin C.;
RT "DAG, a gene required for chloroplast differentiation and palisade
RT development in Antirrhinum majus.";
RL EMBL J. 15:4194-4207(1996).
CC -1- FUNCTION: ACTS VERY EARLY IN CHLOROPLAST DEVELOPMENT, BRING
CC REQUIRED FOR EXPRESSION OF RNA POLYMERASE BETA SUBUNIT GENE, AND
CC HENCE INDIRECTLY FOR SUBSEQUENT EXPRESSION OF CAB AND RBGS GENES.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LEAVES, FLOWERS INCLUDING PETALS,
CC AND TO A LOW LEVEL IN ROOTS.
CC -1- MISCELLANEOUS: EXPRESSION DETECTED IN THE DARK, BUT ENHANCED BY
CC LIGHT.
CC -----
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CC -----
CC EMBL; X95753; CAA65064.1; -
DR PIR; S71747; S71747.
KM Chloroplast; Transit peptide.
FT TRANSIT 1 55
FT CHAIN 56 230 DAG PROTEIN.
FT DOMAIN 66 71 POLY-ASN.
SQ SEQUENCE 230 AA; 25852 MW; CDB33CEBD8DD465 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 230;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1221 EETSEKF 1227

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Db 145 EETSEKF 151
|||||
RESULT 38
ARAD_BACHD . STANDARD; PRT; 231 AA.
ID ARAD_BACHD . STANDARD; PRT; 231 AA.
AC Q9XEQ4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-phosphatase-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose
DE isomerase).
GN ARAD OR BH1871.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=86665;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogatawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-
CC phosphate.
CC -1- COFACTOR: Binds one zinc ion per molecule (Potential).
CC -1- PATHWAY: L-arabinose catabolism; third step.
CC -1- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; AP001513; BAB05590.1; -
DR PIR; G83883; G83883.
DR Interpro: IPR001303; Aldolase_II_N.
DR Pfam: PF00596; Aldolase_II; 1.
KW Arabinose catabolism; Isomerase; Zinc; Complete proteome.
FT METAL 75 75 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 96 96 ZINC (BY SIMILARITY).
FT METAL 168 168 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25991 MW; 6CA570D2A6B4DB97 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 231;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1109 VDLEGNI 1115
Db 59 VDLEGNI 65
|||||
RESULT 39
SMY_MOUSE . STANDARD; PRT; 232 AA.
ID SMY_MOUSE . STANDARD; PRT; 232 AA.
AC P13675;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Y-linked testis-specific protein.
GN SMY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DR Pfam; PF02513; Spin-Saty; 3.  
 KW Developmental protein; Phosphorylation; Cell cycle.  
 FT MOD\_RES 201 201 PHOSPHORYLATION (POTENTIAL).  
 FT MOD\_RES 229 229 PHOSPHORYLATION (POTENTIAL).  
 SQ SEQUENCE 237 AA; 27077 MW; 92267246985712CB CRC64;

Query Match 0.5%; Score 7; DB 1; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 LDDYKE 555  
 DB 156 LDDYKE 162

## RESULT 42

CALD\_MELGA STANDARD; PRT; 239 AA.  
 AC P13505;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Caldesmon, smooth muscle (CDM) (Fragment).  
 GN CALDI OR CAD.  
 OS Meleagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archaeopteryx; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
 NX NCBI\_TaxId=9103;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=gizzard;  
 RX MEDLINE=89273603; PubMed=2730648;  
 RA Leszyk J., Mornet D., Audemard E., Collins J.H.;  
 RT "Caldesmon structure and function: sequence analysis of a 35  
 RT kilodalton actin- and calmodulin-binding fragment from the C-terminus  
 RT of the turkey gizzard protein.";  
 RL Biochem. Biophys. Res. Commun. 160:1371-1378(1989).  
 RN [2]  
 RP SEQUENCE OF 1-96.

RC TISSUE=gizzard;  
 RX MEDLINE=89228015; PubMed=2653315;  
 RA Leszyk J., Mornet D., Audemard E., Collins J.H.;  
 RT "Amino acid sequence of a 15 kilodalton actin-binding fragment of  
 RT turkey gizzard caldesmon: similarity with dystrophin, tropomyosin and  
 RT the tropomyosin-binding region of tropomyosin T.";  
 RL Biochem. Biophys. Res. Commun. 160:210-216(1989).  
 CC -1- FUNCTION: CONTROL OF ACTOMYOSIN INTERACTIONS IN SMOOTH MUSCLE  
 CC AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN AND  
 CC ACTIN FILAMENTS). INHIBITS THE ACTIN-ACTIVATED ATPASE OF MYOSIN  
 CC THIS INHIBITION IS ATTENUATED BY CALCIUM-CALMODULIN AND IS  
 CC POTENTIATED BY TROPOMYOSIN. INTERACTS WITH ACTIN, MYOSIN,  
 CC 2 MOLECULES OF TROPOMYOSIN AND WITH CALMODULIN.  
 CC -1- SUBCELLULAR LOCATION: ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON  
 CC STRESS FIBERS IN FIBROBLASTS (NONMUSCLE).  
 CC PIR; S16925; S16925.  
 DR InterPro: IPR006017; Caldesmon.  
 DR InterPro: IPR006018; Caldesmon\_LSP.  
 DR Pfam; PF02029; Caldesmon; 1.  
 DR PRINTS; PR01076; CALDESMON.  
 KW Muscle protein; Actin-binding; Calmodulin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 239 239  
 SQ SEQUENCE 239 AA; 26561 MW; D395B8BB465B8895 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LDEEOK 44  
 DB 41 LDEEOK 47

## RESULT 43

SPIN\_MOUSE STANDARD; PRT; 240 AA.  
 AC 061142;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Spindlin (30000 Mr metaphase complex) (SSC P).  
 GN SPIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxId=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X DBA/2; TISSUE=Embryo;  
 RX MEDLINE=97178984; PubMed=9053325;  
 RA Oh B., Hwang S.Y., Solter D., Knowles B.B.;  
 RT "Spindlin, a major maternal transcript expressed in the mouse during  
 RT the transition from oocyte to embryo.";  
 RL Development 124:493-503(1997).  
 CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN CELL-CYCLE REGULATION DURING  
 CC THE TRANSITION FROM GAMETE TO EMBRYO.  
 CC -1- SUBCELLULAR LOCATION: ASSOCIATES WITH THE MEIOTIC SPINDLE.  
 CC -1- TISSUE SPECIFICITY: OOCYTE, EGG, AND VERY EARLY EMBRYO; NOT IN THE  
 CC 8-, AND 16-CELL STAGE OF THE EMBRYO.  
 CC -1- DEVELOPMENTAL STAGE: GAMETOGENESIS. SYNTHESIZED FROM MATERNAL  
 CC TRANSCRIPTS BUT NOT FROM THE ZYGOTE GENOME.  
 CC -1- PTM: PHOSPHORYLATION DURING OOCYTE MEIOTIC MATURATION.  
 CC -1- PTM: POST-TRANSLATIONALLY MODIFIED DURING THE FIRST MITOTIC CELL  
 CC CYCLE.

CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.  
 CC  
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 CC  
 CC EMBL; U48972; AAA91233.1; -.  
 DR MGD; MGI:109242; Spin.  
 DR InterPro: IPR003671; Spin\_Saty.  
 DR Pfam; PF02513; Spin-Saty; 3.  
 KW Developmental protein; Phosphorylation; Cell cycle.  
 FT MOD\_RES 204 204 PHOSPHORYLATION (POTENTIAL).  
 FT MOD\_RES 232 232 PHOSPHORYLATION (POTENTIAL).  
 SQ SEQUENCE 240 AA; 27136 MW; D48F03847E8CF876 CRC64;

Query Match 0.5%; Score 7; DB 1; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 LDDYKE 555  
 DB 159 LDDYKE 165

RESULT 44  
 CODY\_CLOPE STANDARD; PRT; 258 AA.  
 ID CODY\_CLOPE  
 AC 08XJ05;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE GTP-sensing transcriptional pleiotropic repressor cody.  
 GN CODY OR CPB1701.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 NX NCBI\_TaxId=1502;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shima T., Ohnami K., Hiraoka H., Oshima K., Yamashita A.,  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RL fresh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- FUNCTION: DNA-binding protein that represses the expression of  
 CC many genes that are induced as cells make the transition from  
 CC rapid exponential growth to stationary phase (By similarity). It  
 CC is a GTP-binding protein that senses the intracellular GTP  
 CC concentration as an indicator of nutritional limitations. At low  
 CC GTP concentration it no longer binds GTP and stop to act as a  
 CC transcriptional repressor (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the cody family.  
 CC -----  
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 CC -----  
 DR EMBL: AB003191; BAB81407.1; -  
 DR HAMAP: MF\_00621; -1;  
 KW Transcription regulation; Repressor; DNA-binding; GTP-binding;  
 FT Complete proteome.  
 PT DNA\_BIND  
 SQ SEQUENCE 258 AA; 28546 MW; E697D3570F83D11 CRC64;  
 H-T-H MOTIF (POTENTIAL).  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 1; Length 258;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 706 EFNDDEL 712  
 DB 135 EFNDDEL 141

RESULT 45  
 SPIN2\_HUMAN  
 ID SPIN2\_HUMAN STANDARD; PRT; 258 AA.  
 AC 09BPZ;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Spindlin-like protein 2 (SPIN-2).  
 GN SPIN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RP Fletcher B.S.;  
 RT "SPIN2, a gene that prevents apoptosis following growth factor  
 RL withdrawal.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heich F.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Anti-apoptotic protein; overexpression causes G2/M  
 CC arrest.  
 CC -1- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF356353; AAK37566.1; -  
 DR EMBL: BC000044; AAH00044.1; -  
 DR InterPro: IPR003671; Spin\_Seq.  
 DR Pfam: PF02513; Spin\_Seq; 3.  
 KW Apoptosis.  
 SQ SEQUENCE 258 AA; 29158 MW; CAD74289970B4BCD CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 7; DB 1; Length 258;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 549 LLDYKE 555  
 DB 177 LLDYKE 183

RESULT 46  
 MOB2\_YEAST  
 ID MOB2\_YEAST STANDARD; PRT; 259 AA.  
 AC P43563;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Maintenance of ploidy protein MOB2 (Mps1 binder 2).  
 GN MOB2 OR YF035C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;  
 ON NCBI\_TaxID=4932;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=S288C / AB972;  
 RX MEDLINE=95400292; PubMed=7670463;  
 RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,  
 RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,  
 RA Yamanaka M., Tashiro H., Eki T.,  
 RT "Analysis of the nucleotide sequence of chromosome VI from  
 RL Saccharomyces cerevisiae.";  
 RL Nat. Genet. 10:261-268(1995).  
 CC -1- SIMILARITY: BELONGS TO THE MOB1/PHOCEIN FAMILY.  
 CC -----  
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DR EMBL; D50617; BAA09204.1; -.
DR PIR; S58648; S58648.
DR SGD; S0001859; MOB2.
DR GO; GO:0005935; C:bud neck; IDA.
DR GO; GO:0005634; C:nuclous; IDA.
DR GO; GO:0030295; P:protein kinase activator activity; IDA.
DR GO; GO:0030012; P:establishment and/or maintenance of cell po. .; IMP.
DR GO; GO:0007096; P:exit from mitosis; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR005301; Mob1_phocoin.
DR Pfam; PF03637; Mob1_phocoin; 1.
DR SEQUENCE 259 AA; 30112 MW; 1. FD45D953AFCEB2282 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 259;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 RLRLRNK 679
DB 14 RLRLRNK 20

RESULT 47
CCG6_HUMAN STANDARD; PRT; 260 AA.
AC Q9BXI2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Voltage-dependent calcium channel gamma-6 subunit (Neuronal voltage-
DE gated calcium channel gamma-6 subunit).
GN CACNG6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100909; PubMed=1170751;
RA Burgess D.L., Gefrides L.A., Foreman P.J., Noebels J.L.;
RT "A cluster of three novel Ca(2+) channel gamma subunit genes on
RT chromosome 19q13.4: evolution and expression profile of the gamma
RT subunit gene family";
RL Genomics 71:339-350(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601102; PubMed=11738816;
RA Chu P.-J., Robertson H.M., Best P.M.;
RT "Calcium channel gamma subunits provide insights into the evolution of
RT this gene family";
RL Gene 280:37-48(2001).
CC -I- FUNCTION: THOUGHT TO STABILIZE THE CALCIUM CHANNEL IN AN
CC INACTIVATED (CLOSED) STATE (BY SIMILARITY).
CC -I- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FIVE SUBUNITS:
CC ALPHA-1, ALPHA-2/Delta, BETA AND GAMMA.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: BELONGS TO THE PMP-22 / EMP / MP20 FAMILY. CACNG
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF288386; AAK20029.1; -.
DR EMBL; AF361352; AAL50047.1; -.
DR Genew; HGNC:13625; CACNG6.
DR MIM; 606898; -.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; NAS.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; NAS.

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DR GO; GO:0006816; P:calcium ion transport; NAS.
DR KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 169 189 POTENTIAL.
FT TRANSMEM 221 241 POTENTIAL.
SQ SEQUENCE 260 AA; 28129 MW; 674433E331FD9974 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 260;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1072 LLLTLPs 1078
DB 239 LLLTLPs 245

RESULT 48
CCG6_MOUSE STANDARD; PRT; 260 AA.
AC Q9VHW3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Voltage-dependent calcium channel gamma-6 subunit (Neuronal voltage-
DE gated calcium channel gamma-6 subunit).
GN CACNG6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=21601102; PubMed=11738816;
RA Chu P.-J., Robertson H.M., Best P.M.;
RT "Calcium channel gamma subunits provide insights into the evolution of
RT this gene family";
RL Gene 280:37-48(2001).
CC -I- FUNCTION: THOUGHT TO STABILIZE THE CALCIUM CHANNEL IN AN
CC INACTIVATED (CLOSED) STATE (BY SIMILARITY).
CC -I- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FIVE SUBUNITS:
CC ALPHA-1, ALPHA-2/Delta, BETA AND GAMMA.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- TISSUE SPECIFICITY: Highly expressed in muscle.
CC -I- SIMILARITY: BELONGS TO THE PMP-22 / EMP / MP20 FAMILY. CACNG
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF361348; AAL50043.1; -.
DR MGD; MGI:1859168; Cacng6.
DR KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 169 189 POTENTIAL.
FT TRANSMEM 221 241 POTENTIAL.
SQ SEQUENCE 260 AA; 28145 MW; 583C326BEB88C80 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 260;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1072 LLLTLPs 1078
DB 239 LLLTLPs 245

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RESULT: 50	
CODY_STRMU	
ID	STANDARD;
AC	PRT; 261 AA.
589368;	
28-FEB-2003	(Rel. 41, Created)

RESULT	51
ID	ARO_NEIMU
AC	ARO_NEIMU
AC	P95389;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Shikimate 5-dehydrogenase (EC 1.1.1.25).
GN	ARO.
OS	Neisseria mucosa.
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC	Neisseriaceae; Neisseria.
NCBI	taxid=488;
NRX	[1]
RRP	SEQUENCE FROM N.A.
RRC	STRAIN=LMP 405;
RKA	MEDLINE=97206157; PubMed=9157250;
RXA	Zhou J., Bowler L.D., Spratt B.G.;
RTT	"interspecies recombination, and phylogenetic distortions, within the
RTT	glutamine synthetase and shikimate dehydrogenase genes of <i>Neisseria</i>
RTT	meningitidis and commensal <i>Neisseria</i> species.";



RL Mol. Microbiol. 23:799-812(1997).  
 CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +  
 CC NADPH.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC fourth step.  
 CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.  
 CC  
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 CC  
 CC EMBL; U82848; AAC4919.1; -.  
 DR HAMAP; MF\_00222; -; 1.  
 DR InterPro; IPR006152; Shikimate.  
 DR InterPro; IPR006151; Shikimate.DH.  
 DR Pfam; PF01488; Shikimate.DH; 1.  
 DR TIGRPFAM; TIGR00507; ar05; 1.  
 DR KW Aromatic amino acid biosynthesis; Oxidoreductase; NADP.  
 SQ SEQUENCE 269 AA; 28628 MW; 0908539F2BB5957P CRC64;  
  
 Query Match 0.5%; Score 7; DB 1; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 474 SGTIVL 480  
 DB 122 SGTIVL 128  
  
 RESULT 52  
 ID Y0AC\_LACIA STANDARD; PRT; 281 AA.  
 AC 09CFB9;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical UPF0230 protein y0ac.  
 GN Y0AC OR IL1562.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IL1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malame K.,  
 RA Weisenbach J., Ehrlich S.D., Sorokin A.;  
 RT The complete genome sequence of the lactic acid bacterium Lactococcus  
 RT lactis ssp. lactis IL1403.";  
 RL Genome Res. 11:731-753(2001).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0230 (DEGV) FAMILY.  
 CC  
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 CC  
 CC EMBL; AE006387; AAK05660.1; -.  
 DR PIR; B86820; B86820.  
 DR InterPro; IPR003797; DegV.  
 DR Pfam; PF02645; DUF194; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 281 AA; 31816 MW; 370A993314PDC59 CRC64;  
  
 Query Match 0.5%; Score 7; DB 1; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 711 DLBAGV 717  
 DB 132 DLBAGV 138  
  
 RESULT 53  
 ID MRP\_CLOPE STANDARD; PRT; 284 AA.  
 AC P53181;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE MRP protein homolog.  
 DE MRP OR CPB2512.  
 GN MRP OR CPB2512.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Onohima K., Yamashita A.,  
 RA Shiba T., Ogawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 RN [2]  
 RP SEQUENCE OF 50-189 FROM N.A.  
 RC STRAIN=CPN50;  
 RX MEDLINE=96032407; PubMed=7559358;  
 RA Katayama S.-I., Dupuy B., Garnier T., Cole S.T.;  
 RT "Rapid expansion of the physical and genetic map of the chromosome of  
 RT Clostridium perfringens CPN50.";  
 RL J. Bacteriol. 177:5680-5685(1995).  
 CC -1- FUNCTION: NOT KNOWN.  
 CC -1- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING  
 CC PROTEINS.  
 CC  
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 CC  
 CC EMBL; AP003194; BAB82218.1; -.  
 DR EMBL; X86509; CA60227.1; -.  
 DR InterPro; IPR000808; MRP\_family.  
 DR PROSITE; PS01215; MRP; 1.  
 KW ATP-binding; Complete proteome.  
 FT NP BIND 46 53 ATP (POTENTIAL).  
 SQ SEQUENCE 284 AA; 30835 MW; 8CB32FBBF0510EAP CRC64;  
  
 Query Match 0.5%; Score 7; DB 1; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 229 SKKSSSE 235  
 DB 232 SKKSSSE 238  
  
 RESULT 54  
 ID TAP1\_NPVAC STANDARD; PRT; 286 AA.  
 AC P41435;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Apoptosis inhibitor 1 (IAP-1).  
 GN IAP1.  
 OS Autographa californica nuclear polyhedrosis virus (AcMNPV).  
 OC Viruses; deDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 RX NCBI\_TaxId=46015;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C6;  
 RA MEDLINE=94303173; PubMed=8030224;  
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;  
 RT "The complete DNA sequence of Autographa californica nuclear  
 RT polyhedrosis virus.";  
 RL Virology 202:586-605 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E2;  
 RA MEDLINE=93079853; PubMed=133113;  
 RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,  
 RT "Sequence, genomic organization of the EcoRI-A fragment of Autographa  
 RT californica nuclear polyhedrosis virus, and identification of a  
 RT viral-encoded protein resembling the outer capsid protein VP8 of  
 RT rotavirus.";  
 RL Virology 191:1003-1008 (1992).  
 CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY  
 CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.  
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.  
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 DR EMBL; L22858; AAA66557.1; -;  
 DR EMBL; M96361; AAA66796.1; -;  
 DR PIR; D36828; D36828;  
 DR HSSP; Q13490; 10BH.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001841; Znf\_fing.  
 DR Pfam; PF00653; BIR; 2.  
 DR SMART; SM00238; BIR; 2.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 2.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS0089; ZF\_RING\_2; 1.  
 KM Apoptosis; Zinc-finger; Repeat.  
 FT REPEAT 29 96 BIR 1.  
 FT REPEAT 131 199 BIR 2.  
 FT ZN\_FING 238 274 RING-TYPE  
 SO SEQUENCE 286 AA; 33320 MW; PFES505A35FE1BEA CRC64;  
 Query Match 0.5%; Score 7; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 302 AGLEFYTG 308  
 DB 156 AGLEFYTG 162

DE Zinc finger protein 75.  
 GN ZNF75.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RX NCBI\_TaxId=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung fibroblast;  
 RX MEDLINE=94116987; PubMed=8286223;  
 RA Villa A., Zucchi I., Pilla G., Strina D., Susani L., Morali F.,  
 RA Patrosso C., Fratini A., Lucchini F., Repetto M., Sacco M.G.,  
 RT ZNF75: Isolation of a cDNA clone of the KRAB zinc finger gene  
 RT subfamily mapped in YACs 1 Mb telomeric of HPRT.";  
 RL Genomics 18:223-229 (1993).  
 RN [2]  
 RP SEQUENCE OF 139-289 FROM N.A.  
 RA Martino M., Archidiacono N., Franze N., Rosati M., Rocchi M.,  
 RA Ballabio A., Grimaldi G.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
 CC -1- SIMILARITY: BELONGS TO THE KRUPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC -1- SIMILARITY: Contains 1 KRAB domain.  
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 DR EMBL; S67970; AAB29696.1; -;  
 DR EMBL; X68010; CAA48147.1; -;  
 DR PIR; A48913; A48913.  
 DR HSSP; P25490; 12NM.  
 DR GeneW; HGNC:13145; ZNF75.  
 DR MIM; 314997; -;  
 DR GO; GO:0005634; C:nucleus; NAS.  
 DR GO; GO:0003677; P:DNA binding activity; NAS.  
 DR GO; GO:0008270; F:zinc ion binding activity; NAS.  
 DR GO; GO:000355; P:regulation of transcription; NAS.  
 DR InterPro; IPR001909; KRAB.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF01352; KRAB; 1.  
 DR Pfam; PF00096; ZF-C2H2; 5.  
 DR PRINTS; PR00048; ZINC\_FINGER.  
 DR PRODOM; PD000003; Znf\_C2H2; 3.  
 DR SMART; SM00349; KRAB; 1.  
 DR SMART; SM00355; ZNF\_C2H2; 5.  
 DR PROSITE; PS08005; KRAB; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 5.  
 DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 5.  
 KM Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 FT DOMAIN 14 97 KRAB.  
 FT ZN\_FING 144 166 C2H2-TYPE 1.  
 FT ZN\_FING 172 194 C2H2-TYPE 2.  
 FT ZN\_FING 200 222 C2H2-TYPE 3.  
 FT ZN\_FING 228 250 C2H2-TYPE 4.  
 FT ZN\_FING 256 278 C2H2-TYPE 5.  
 SO SEQUENCE 289 AA; 33683 MW; 96E7B008F1DF64DE CRC64;  
 Query Match 0.5%; Score 7; DB 1; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 907 PSLSL 913

Db 8 PESTSL 14

RESULT 56

MEF\_BUCAP STANDARD; PRT; 292 AA.

AC 08K62;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 5,10-methyltetrahydrofolate reductase (EC 1.7.99.5).

GN MEF OR BUC043.

OS Buchnera aphidicola (subsp. Schizaphis graminum).

OC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.

NCBI\_TaxID=98794;

OK NCB1

RP SEQUENCE FROM N.A.

RA MEDLINE=22084549; PubMed=12089438;

RA Tams I., Klason L., Canback B., Naeslund A.K., Eriksson A.-S., Wernegreen J.U., Sandstrom J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic Bacteria."; Science 296:2376-2379(2002).

RT -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + acceptor = 5,10-methylenetetrahydrofolate + reduced acceptor.

CC -1- COFACTOR: PAD (By similarity).

CC -1- PATHWAY: Methionine biosynthesis.

CC -1- SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.

CC -----

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CC -----

DR EMBL: AE014080; AAM67614.1; -

DR InterPro: IPR004620; Pfam2\_Bact.

DR InterPro: IPR003171; Methylrof\_redctse.

DR Pfam: PF02219; MTHFR; 1.

DR TIGRFAMs: TIGR00676; fadh2; 1.

KM Oxidoreductase; Flavoprotein; PAD; Methionine biosynthesis; Complete proteome.

KW SEQUENCE 292 AA; 33676 MW; 0660895E1B065E71 CRC64;

SQ

Query Match 0.5%; Score 7; DB 1; Length 292;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 VLLKKIA 484

Db 137 VLLKKIA 143

RESULT 57

RSEC MYXXA STANDARD; PRT; 295 AA.

ID RPSC MYXXA

AC 007083;

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DE 01-FEB-1995 (Rel. 31, Last annotation update)

DE RNA polymerase sigma-C factor.

GN SIGC.

OS Myxococcus xanthus.

OC Bacteria: Proteobacteria; Deltaproteobacteria; Myxococcales; Cytochromatellaceae; Myxococcaceae; Myxococcus.

NCBI\_TaxID=34;

OK NCB1

RP SEQUENCE FROM N.A.

RA STRAIN=FB / DZFL1;

RX MEDLINE=93273699; PubMed=8501037;

RA Apelian D., Inouye S.;

RT "A new putative sigma factor of Myxococcus xanthus.";

RL J. Bacteriol. 175:3335-3342(1993)

CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED. THIS SIGMA FACTOR IS ESSENTIAL FOR NORMAL FRUITING BODY FORMATION.

CC -1- SIMILARITY: Belongs to the sigma-70 factor family.

CC -----

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CC -----

DR EMBL: U12992; AAA25408.1; -

DR PIR: A40587; A40587.

DR HSSP: P00579; 1SIG.

DR InterPro: IPR000943; Sigma\_70.

DR Pfam: PF00140; sigma70\_r1\_2; 1.

DR Pfam: PF04542; sigma70\_r2; 1.

DR Pfam: PF04539; sigma70\_r3; 1.

DR Pfam: PF04545; sigma70\_r4; 1.

DR PRINTS: PR00046; SIGMA70FCT.

DR PROSITE: PS00715; SIGMA70\_1; FALSE NEG.

DR PROSITE: PS00716; SIGMA70\_2; FALSE NEG.

KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase; DNA-binding.

FT DOMAIN 73 86 POLYMERASE CORE BINDING (POTENTIAL).

FT DNA\_BIND 250 269 H-T-H MOTIF (BY SIMILARITY).

SQ SEQUENCE 295 AA; 33433 MW; DB2D4E783C7BA49 CRC64;

QY 713 AEAQYDE 719

Db 284 AEAQYDE 290

RESULT 58

Y326 MYCGE STANDARD; PRT; 295 AA.

ID Y326 MYCGE

AC P47568;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Hypothetical UPF0230 protein MG326.

GN MG326.

OS Mycoplasma genitalium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

NCBI\_TaxID=2097;

OK NCB1

RP SEQUENCE FROM N.A.

RA STRAIN=ATCC 33530 / G-37;

RC MEDLINE=96026346; PubMed=7569993;

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fumrman J.L., Nguyen D.T., Ullrich J.R., Sander D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.";

RT Science 270:397-403(1995).

CC -1- SIMILARITY: BELONGS TO THE UPF0230 (DEGV) FAMILY.

CC -----

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CC -----
DR EMBL/ U93714; AAC71550.1; -
DR PIR/ A64236; A64236.
DR TIGR/ MG326; A64236.
DR InterPro: IPR003797; DegV.
DR Pfam: PF02645; DUF194; 1.
DR TIGRfam: TIGR00762; DegV; 1.
KW Hypothetical protein; Complete proteome.
SQ
SEQUENCE 295 AA; 33413 MW; 04610881C0F841EE CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 295;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 VOLAKEL 38
DB 102 VOLAKEL 108

RESULT 59
NIPD NOSCO STANDARD; PRT; 296 AA.
ID NIPD NOSCO
AC P52337;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)
GN NIPD.
OS Nostoc commune.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=1178;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX 584;
RA MEDLINE=94341563; Pubmed=8063099;
RA Angeloni S.V., Potte M.;
RT "Analysis of the sequences within and flanking the
RT cyanoglobin-encoding gene, glbN, of the cyanobacterium Nostoc commune
RT UTEX 584";
RL Gene 146133-134(1994).
CC
CC -1- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -1- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
CC 30-32 FE, 2 MO, AND INORGANIC SULFUR.
CC -1- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
CC
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CC -----
DR EMBL/ L25514; AAA21839.1; -
DR HSPB/ P07328; 3MIN.
DR InterPro: IPR00318; Nitrogenase comp1.
DR Pfam: PF00148; oxidized nifH; 1.
DR PROSITE: PS00090; NITROGENASE_1_2; 1.
DR PROSITE: PS00099; NITROGENASE_1_1; 1.
KW Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
FT NON TER
SQ
SEQUENCE 296 AA; 32987 MW; 3E061E67B8FDF382 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 296;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1146 KLVKLQ 1152
DB 132 KLVKLQ 138

RESULT 60
BIR7 HUMAN STANDARD; PRT; 298 AA.
ID BIR7 HUMAN
AC 096C85; Q9BQV0; Q9H2A8; Q9HAP7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 7 (kidney inhibitor of
DE apoptosis protein) (KIAP) (Melanoma inhibitor of apoptosis protein)
DE (ML-IAP) (Ivlin).
GN BIR7 OR KIAP OR ML-IAP OR LIVIN.
OS Homo sapiens (human).
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal kidney;
RX MEDLINE=21092523; Pubmed=11162435;
RA Lin J.-H., Deng G., Huang Q., Morser J.;
RT "KIAP, a novel member of the inhibitor of apoptosis protein family";
RL Biochem. Biophys. Res. Commun. 279:820-831(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=2123043; Pubmed=1132947;
RA Ashhab Y., Allan A., Pollack A., Panet A., Yehuda D.B.;
RT "Two splicing variants of a new inhibitor of apoptosis gene with
RT different biological properties and tissue distribution pattern.";
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=11024045;
RA Kaeo G.M., Gomes B.C.;
RT "Livin, a novel inhibitor of apoptosis protein family member.";
RL J. Biol. Chem. 276:3238-3246(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21638749; Pubmed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corry N.R.,
RA Coulson A.G., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A., Frankland J.A., Fraser M.N.D., Gwilliam R., Hall R.E.,
RA Hammond D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Johnson C.M., Johnson D.,
RA Lehar V.L., Martin S.L., Levesha M.A., Lloyd C., Lloyd G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Munnell J.C., Murray A.A.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pratchalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Selva R.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.M., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams L.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

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RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
[5]  
RN SEQUENCE FROM N.A. (ISOFORM 2).  
RP  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshynki S., Cantini P., Prange C.,  
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M.,  
RA Butcherfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,  
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RN FUNCTION, AND MUTAGENESIS OF GLU-87; GLU-88; CYS-124; ASP-120 AND  
RP ASP-138.  
RX MEDLINE=20538921; PubMed=11084335;  
RA Vucic D., Steniche H.R., Pisabarro M.T., Salveen G.S., Dixit V.M.;  
RT "ML-1AP, a novel inhibitor of apoptosis that is preferentially  
expressed in human melanoma.";  
RL Curr. Biol. 10:1359-1366(2000).  
[7]  
RN INTERACTION WITH SMAC.  
RP MEDLINE=21922807; PubMed=11801603;  
RA Vucic D., Deshayes K., Ackerly H., Pisabarro M.T., Kaddhodayan S.,  
RA Fairbrother W.J., Dixit V.M.;  
RT "SMAC negatively regulates the anti-apoptotic activity of melanoma  
inhibitor of apoptosis (ML-1AP).";  
RL J. Biol. Chem. 277:12275-12279(2002).  
[8]  
RN ACTIVATION OF MAP KINASES.  
RP MEDLINE=21853687; PubMed=11965055;  
RA Samra M.G., da Silva Correia J., Ducey O., Lee J., Nomoto K.,  
RA Schantz N., Deveraux Q.L., Ulevitch R.J.;  
RT "MAP suppression of apoptosis involves distinct mechanisms: the  
TAK1/JNK1 signaling cascade and caspase inhibition.";  
RL Mol. Cell. Biol. 22:1154-1166(2002).  
-1- FUNCTION: Protects against apoptosis induced by TNF or by chemical  
agents such as adriamycin, etoposide or staurosporine. Suppression  
of apoptosis is mediated by activation of MAPK/JNK1, and possibly  
also of MAPK9/JNK2. This activation depends on TAK1 and  
MK2C/TAK1. In vitro, inhibits caspase-3 and proteolytic  
activation of pro-caspase-9. Isoform 1 blocks staurosporine-  
induced apoptosis and isoform 2 blocks etoposide-induced  
apoptosis.  
CC -1- SUBUNIT: Binds to caspase-9. Interaction with SMAC via the BIR  
CC domain disrupts binding to caspase-9 and apoptotic suppressor  
CC activity. Interacts with TAK1. In vitro, interacts with caspase-3  
CC and caspase-7 via its BIR domain.  
CC -1- SUBCELLULAR LOCATION: Nuclear, and in a filamentous pattern  
CC throughout the cytoplasm.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing, Named isoforms=3;  
CC Name=2; Synonyms=Livin alpha;  
CC IsoId=Q96CA5-1; Sequence=Displayed;  
CC Name=1; Synonyms=Livin beta;  
CC IsoId=Q96CA5-2; Sequence=VSP\_002459;  
CC Name=3;  
CC IsoId=Q96CA5-3; Sequence=VSP\_002458;

CC	-1- TISSUE SPECIFICITY: Very low levels or not detectable in most adult tissues. Detected in adult heart, placenta, lung, lymph node, spleen and ovary, and in several carcinoma cell lines (isoforms 1 and 2). Isoform 2 (but not isoform 1) is detected in fetal kidney, heart and spleen, and at lower levels in adult brain, skeletal muscle and peripheral blood leukocytes.
CC	-1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC	-1- SIMILARITY: Contains 1 BIR repeat.
CC	-1- SIMILARITY: Contains 1 RING-type zinc finger.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .
CC	-----
DR	EMBL; AF301009; AAC37878.1; -
DR	EMBL; AJ309298; CAC37337.1; -
DR	EMBL; AJ309298; CAC37338.1; -
DR	EMBL; AF311388; AAC33622.1; -
DR	EMBL; ALJ21827; CAC36111.1; -
DR	EMBL; ALJ21827; CAC36112.1; -
DR	EMBL; ALJ21827; CAC36113.1; ALT_INT.
DR	EMBL; BC014475; AAH14475.1; -
DR	PIR; JCT568; JCT568.
DR	HSSP; Q13490; IQBH.
DR	Genew; HGNC:13702; BIRC7.
DR	MIM; 605737; -
DR	GO; GO:0005622; C:intracellular; IC.
DR	GO; GO:0008189; F:apoptosis inhibitor activity; NAS.
DR	GO; GO:0019899; F:enzyme binding activity; NAS.
DR	GO; GO:0007257; P:activation of JUN kinase; NAS.
DR	GO; GO:0006309; P:DNA fragmentation; NAS.
DR	GO; GO:0001719; P:inhibition of caspase activation; IEP.
DR	Interpro; IPRO01370; BIR.
DR	Interpro; IPRO01841; Znf_fing.
DR	Pfam; PF00653; BIR; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 1.
DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01262; BIR_REPEAT_1; 1.
DR	PROSITE; PS0143; BIR_REPEAT_2; 1.
DR	PROSITE; PS00518; zf_RING_1; 1.
DR	PROSITE; PSS0089; zf_RING_2; 1.
KW	Apoptosis; Zinc-finger; Alternative splicing.
REPEAT	90 155
FT	ZN_FING 252 286
FT	DOMAIN 64 69
VARSPLIC	1 149
FT	VARSPPLIC
FT	VARSPPLIC 216 233
FT	MUTAGEN 87 88
FT	MUTAGEN 120 120
FT	MUTAGEN 124 124
FT	
Query Match	0.5%; Score 7; DB 1; Length 298;
Best Local Similarity	100.0%; Pred. No. 1.3e+02;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	216 EHAKWP 222
DB	143 EHAKWP 149

```

RESULT 61
GLXB RHIME
ID GLXB RHIME STANDARD; PRT; 300 AA.
AC 067350;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Glutamine amidotransferase-like protein glxb.
OS GLXB OR R00087 OR SMC02610.
OC Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxId=382;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RL Powers E.L., Vuyuru V., Kahn M.L.;
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Couzy J., Bothe G., Ampe F., Batut J.,
RA Boizard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godtke T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masny D.,
RA Pohl T., Portetalle D., Puehler A., Purnelle B., Rampeger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF055582; AAC62220.1; ALT INIT.
DR EMBL; AL591782; CAC41474.1; ALT INIT.
DR InterPro; IPR000583; GATase.2.
DR Pfam; PF00310; GATase.2.1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Transferrase; Glutamine amidotransferase; Complete proteome.
FT INIT MET 0 BY SIMILARITY.
FT ACT SITE 1 GATASE (BY SIMILARITY).
SQ SEQUENCE 300 AA; 31987 MW; 985968489509248 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 711 DLAEAGV 717
DB 68 DLAEAGV 74

RESULT 62
HEMK MYCTU
ID HEMK MYCTU STANDARD; PRT; 304 AA.
AC Q10602;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hemk protein homolog (EC 2.1.1.-) (M. MtuHemKp).
GN HEMK OR RV1300 OR MT1330 OR MTCY373.20.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxId=11964;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleisemann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Desoy R., Dodson R., Gwin M.L., Hatt D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Enolaeva M.D., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Knout H., Gill J., Mikula A.,
RA Bishop W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE HEMK FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; Z73119; CAA97733.1; ALT INIT.
DR EMBL; AE007008; AAK45601.1;
DR REBASE; 4465; M.MtuHemKp.
DR TIGR; MT1339;
DR TubercuList; RV1300;
DR InterPro; IPR004556; Hemk.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000051; SAM_bind.
DR TIGRFAMs; TIGR00536; hemk_fam; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW Transferrase; Methyltransferase; Complete proteome.
FT CONFLICT 173 173 R -> C (IN REF. 2).
SQ SEQUENCE 304 AA; 32459 MW; 66CFA72FD2EA3455 CRC64;
Query Match 0.5%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 712 LAEAGVD 718
DB 14 LAEAGVD 20

RESULT 63
BE11 SFV1
ID BE11 SFV1 STANDARD; PRT; 308 AA.
AC P29169;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUN-1993 (Rel. 26, Last sequence update)
DE BEV-1 protein.
GN BEV-1 OR TAF.
OS Simian foamy virus (type 1) (SFV-1).
OC Viruses; Retroviridae; Retroviridae; Spumavirus.
OX NCBI_TaxId=11964;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=91276270; PubMed=1647358;
RA Kupiec J.-J., Kay A., Hayat M., Ravier R., Peries J., Gallibert F.;
RT "Sequence analysis of the simian foamy virus type 1 genome.";
RL Gene 101:185-194(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9127804; PubMed=1851862;
RA Merga A., Shaw K.E.S., Pratt-Lowe E., Barry P.A., Luciw P.A.;
RT "Identification of the simian foamy virus transcripional
transactivator gene (taf)";
RL J. Virol. 65:2903-2909(1991).
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTIONAL TRANSACTIVATOR.
CC -----
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CC -----
DR EMBL; X51482; -; NOT ANNOTATED_CDS.
DR EMBL; W74039; AAA47802.1; -.
DR PIR; B39924; WMLJ51.
DR InterPro; IPR004956; Foamy BEL.
DR Pfam; PF03274; Foamy BEL; 1.
KW Transcription regulation; Activator.
FT CONFLICT 89 89 D -> N (IN REF. 2).
FT CONFLICT 119 119 D -> N (IN REF. 2).
FT CONFLICT 257 257 S -> G (IN REF. 2).
SQ SEQUENCE 308 AA; 35311 MW; 7E280B6F821D992 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1073 LITLPSL 1079
DB 187 LITLPSL 193

RESULT 64
CITR_BACSU
ID CITR_BACSU STANDARD; PRT; 308 AA.
AC P39127;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Citrate synthase I repressor.
GN CITR
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / SMY;
RA MEDLINE=94321340; PubMed=8045898;
RA Jin S., Sonenshein A.L.;
RT "Identification of two distinct Bacillus subtilis citrate synthase
genes.";
RL J. Bacteriol. 176:4669-4679(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
RA MEDLINE=98240224; PubMed=9579061;
RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.;
RA Medler H., Venema G., Bron S.;
RT "The 172 kb ptkA-addA region from 83 degrees to 97 degrees of the
Bacillus subtilis chromosome contains several dysfunctional genes,
the gylB marker, many genes encoding transporter proteins, and the
ubiquitous hit gene.";
RL Microbiology 144:859-875(1998).

```

```

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunes F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bouillat S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Dancot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Gallizzi A., Galleron N.,
RA Gim S.Y., Glaeser P., Goffeau A., Golighly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Ilaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vanlier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Dancin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
RN [4]
RP FUNCTION.
RX MEDLINE=94321341; PubMed=8045899;
RA Jin S., Sonenshein A.L.;
RT "Transcriptional regulation of Bacillus subtilis citrate synthase
genes.";
RL J. Bacteriol. 176:4680-4690(1994).
CC -1- FUNCTION: NEGATIVE REGULATORY PROTEIN FOR THE CITR GENE FOR
CITRATE SYNTHASE I.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE LYR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
CC -----
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CC -----
DR EMBL; U05256; AAA20935.1; -.
DR EMBL; Y14082; CAA74488.1; -.
DR EMBL; Z99109; CAB12782.1; -.
DR PIR; I40379; I40379.
DR Subtilist; BG10853; Citr.
DR InterPro; IPR000847; HTH_LYR.
DR InterPro; IPR005119; LysR_substc.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS00044; HTH_LYR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Repressor; Complete proteome.
FT DNA BIND 18 37 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 308 AA; 35595 MW; 53B5F866A8F1037 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 107 AGUTRLP 113  
 DB 266 AGUTRLP 272

## RESULT 65

GLSA RHINE  
 ID GLSA RHINE STANDARD; PRT; 315 AA.

AC 092RH0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Glutaminease (EC 3.5.1.2)  
 GN GLSA OR R01786 OR SMC00486.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 CX NCBI\_TaxID=382;  
 RN [1]

## SEQUENCE FROM N.A.

RA STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Bolger D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Bolger D., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Goffe I., Goffeau A., Kahn D., Kiss E., Laizure V., Maury D.,  
 RA Pohl F., Portetelle D., Puehler A., Purnelle B., Rampeger U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.,  
 RA Sinorhizobium meliloti strain 1021.  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 CC -1- CATALYTIC ACTIVITY: L-glutamate + H(2)O = L-glutamate + NH(3).  
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINASE FAMILY

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DR EMBL; AL591788; CAC6365.1; -  
 DR HAMAP; MF\_00313; -; 1.  
 DR InterPro; IPR007043; Glutaminease.  
 DR Pfam; PF04960; Glutaminease; 1.  
 DR KX  
 DR HydroLase; Complete proteome.  
 SO SEQUENCE 315 AA; 33991 MW; C83A62CAB20A2B84 CRC64;

## Query Match

Best Local Similarity 0.5%; Score 7; DB 1; Length 315;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 LAKAGLP 305  
 DB 210 LAKAGLP 216

## RESULT 66

REF4 YEAST  
 ID REF4 YEAST STANDARD; PRT; 323 AA.

AC P40339;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE Activator 1 37 kDa subunit (Replication factor C subunit 4)  
 DE (Replication factor C4)  
 GN RFC4 OR YOL094C OR O0923.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 CX NCBI\_TaxID=4932;  
 RN [1]

## SEQUENCE FROM N.A.

RP STRAIN=M303;  
 RX MEDLINE=94342386; PubMed=8063832;  
 RA Li X., Burgers P.M.J.;  
 RT "Cloning and characterization of the essential Saccharomyces  
 RT cerevisiae RFC4 gene encoding the 37-kDa subunit of replication  
 RT factor C";  
 RL J. Biol. Chem. 269:21880-21884(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RX MEDLINE=95379608; PubMed=7651383;  
 RA Cullman G., Flen K., Kobayashi R., Stillman B.;  
 RT "Characterization of the five replication factor C genes of  
 RT Saccharomyces cerevisiae";  
 RL Mol. Cell. Biol. 15:4661-4671(1995).  
 RN [3]

## SEQUENCE FROM N.A.

RP STRAIN=S288C / FY1679;  
 RX MEDLINE=96021609; PubMed=8533473;  
 RA Zumberg B., Pearson B.M., Kalogetopoulos A., Schweizer M.;  
 RT "A 29,425 kb segment on the left arm of yeast chromosome XV contains  
 RT more than twice as many unknown as known open reading frames";  
 RL Yeast 11:975-986(1995).  
 RN [4]

## SEQUENCE FROM N.A.

RA Dujon B., Albertmann K., Aldea M., Alexandraki D., Ansoorge W.,  
 RA Arino J., Benes V., Bohm C., Bolotin-Fukuhara M., Bordonne R.,  
 RA Boyer J., Camasse A., Casamayor A., Casas C., Charet G.,  
 RA Ciepluch C., Dagnan-Fornier B., Dang D.V., de Haan M., Delius H.,  
 RA Durand F., Fairhead C., Feldmann H., Gallion L., Gallison F.,  
 RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,  
 RA Habbing B., Hand N.J., Han J., Hattendorff U., Hebling U.,  
 RA Herando Y., Herrero E., Henmann K., Hiesel R., Hiltner F., Hofmann B.,  
 RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogetopoulos A.,  
 RA Katsoulou C., Kordeas E., Latuente M.J., Landt O., Louis E.J.,  
 RA Maesse H.-W., Michaux A., Mannhaupt G., Marck C., Martin R.P.,  
 RA Perrin A., Petersson B., Paces V., Parle-McDermott A.G., Pearson B.M.,  
 RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Reckmann S.,  
 RA Schweizer C., Schweizer M., Sor F., Sterky F., Tarasov I.A.,  
 RA Theodoru C., Tettelein H., Thierry A., Tobiasch B., Tzermia M.,  
 RA Thoden M., Unsel M., Valens M., Vandenbol M., Vetter I., Vleck C.,  
 RA Voet M., Volckaert G., Voss H., Wamboldt R., Weidner S., Wiemann S.,  
 RA Winsor B., Wolfe K.H., Zollner A., Zumberg B., Klein K.,  
 RL "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV";  
 RL Nature 387:98-102(1997).

CC -1- FUNCTION: The elongation of primed DNA templates by DNA polymerase  
 CC delta and epsilon requires the action of the accessory proteins  
 CC proliferating cell nuclear antigen (PCNA) and activator 1.  
 CC -1- SUBUNIT: Heteropentamer of subunits RFC1, RFC2, RFC3, RFC4 and  
 CC RFC5 that forms a complex with PCNA in the presence of ATP. RFC4  
 CC forms a tight complex with RFC3.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ACTIVATOR 1 36 TO 40 KDA SUBUNITS  
 CC FAMILY.

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DR EMBL; L20502; AAA34970.1; -  
 DR EMBL; U26030; AAC49063.1; -  
 DR EMBL; X83121; CAA58185.1; -  
 DR EMBL; Z74836; CAA59106.1; -  
 DR PIR; A53845; A53845.  
 DR SGD; S0005454; RFC4.  
 DR GO; GO:0005663; C:DNA replication factor C complex; IDA.





CC -1- SUBUNIT: Could be composed of four subunits: pucA, pucC, pucD and pucE.

CC -1- INDUCTION: Expression is very low in excess nitrogen (glutamate plus ammoniac) and is induced during limiting-nitrogen conditions

CC limiting-nitrogen conditions when allantoic acid is added during limiting-nitrogen conditions.

CC -----

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CC EMBL; 299120, CAB15241.1; -

DR PIR; E70017, E70017.

DR Subtilase; BG13992; pUCA.

DR InterPro; IPR003777, DUF182.

DR Pfam; PF02625; XdhC\_Cox1; 1.

KM Oxidoreductase; NAD; Purine metabolism; Complete proteome.

SO SEQUENCE 330 AA; 36746 MW; E4A70B2155BE1902 CRC64;

Query Match

Best Local Similarity 0.5%; Score 7; DB 1; Length 330;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LILFGAG 108

DB 185 LILFGAG 191

RESULT 69

YB21 YEAST STANDARD; PRT; 337 AA.

AC P38278;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Hypothetical 38.5 kDa protein in IRA1-MAK5 intergenic region.

GN YB1141C OR YB1118.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;

NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=8288c;

RA MEDLINE=95274325; PubMed=754712;

RA Zagulski M., Becan A.-M., Grzybowska E., Lacroite F., Migdalaki A.,

RT "The sequence of 12.5 kb from the right arm of chromosome II predicts a new N-terminal sequence for the IRA1 protein and reveals two new

RL gene, one of which is a DEAD-box helicase.";

Yeast 10:1227-1234 (1994).

CC -----

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CC EMBL; Z36010, CAAB5099.1; -

DR EMBL; X78937, CAAB5538.1; -

DR PIR; S46010; S46010.

DR SCD; S0000345; YBRI41C.

KM Hypothetical protein.

SO SEQUENCE 337 AA; 38539 MW; CB0039B18FABF3BE CRC64;

Query Match

Best Local Similarity 0.5%; Score 7; DB 1; Length 337;

Matches 100.0%; Pred. No. 1.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 KFLCKE 1106

DB 48 KFLCKE 54

RESULT 70

Y042 CLOPE STANDARD; PRT; 337 AA.

AC 08XBD;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical ATP:guanine phosphotransferase CPE2442 (EC 2.7.3.-).

GN CPE2442.

OS Clostridium perfringens.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

NCBI\_TaxID=1502;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;

RA MEDLINE=21664373; PubMed=11792842;

RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

RT Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

RT "Complete genome sequence of Clostridium perfringens, an anaerobic

RL flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).

CC -1- SIMILARITY: BELONGS TO THE ATP:GUANIDO PHOSPHOTRANSFERASE FAMILY.

CC -----

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CC EMBL; AP003194; BA882148.1; -

DR HAMAP; MF\_00602; -; 1.

DR InterPro; IPR000749; ATP-gua\_Pfams.

DR Pfam; PF00217; ATP-gua\_Pfams; 1.

DR PROSITE; PS00112; GUANIDO\_KINASE; FALSE NEG.

KM Hypothetical protein; Transferrase; Kinase; Complete proteome.

SO SEQUENCE 337 AA; 38765 MW; 4BC7C84B11FDAD1 CRC64;

Query Match

Best Local Similarity 0.5%; Score 7; DB 1; Length 337;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 NKDVGN1 135

DB 200 NKDVGN1 206

RESULT 71

TGDS HUMAN STANDARD; PRT; 350 AA.

AC 09455; Q9H179;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE dTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).

GN TGDS.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Scurla L., Bisio A., Zanardi D., De Flora A., Tonetti M.;

RT "Identification of dTDP-D-glucose 4,6 dehydratase in human cells.";

RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Sepala R., Lehto V.-P., Gahl W.A.;  
 RT "Similar to Hemophilus influenzae dTDP-glucose 4,6-dehydratase.";  
 RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stalcenko M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN (4)  
 RP SEQUENCE OF 106-350 FROM N.A.  
 RA Bates K.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-  
 CC glucose + H(2)O.  
 CC -1- COFACTOR: NAD (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTPD-GLUCOSE  
 CC DEHYDRATASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AJ006068; CA06840.1; -  
 CC EMBL: AF048686; AA050061.1; -  
 CC EMBL: BC033675; AA133675.1; -  
 CC EMBL: AL133318; CAC19462.1; -  
 CC HSSP: P27830; IBXK.  
 CC DR HSSP: HSSP:20324; TGSU.  
 CC DR InterPro: IPR001509; Epimerase\_Dh.  
 CC DR Pfam: PF01370; Epimerase; 1.  
 CC KW Lyase; NAD; 40214 MW; EE427AD1D91EA3D CRC64;  
 CC SQ SEQUENCE 350 AA; 40214 MW; EE427AD1D91EA3D CRC64;  
 CC  
 CC Query Match 0.5%; Score 7; DB 1; Length 350;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mannonate dehydratase (EC 4.2.1.8) (D-mannonate hydrolase).  
 GN UXUA OR CPE0151.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 CC NCB1\_TaxID=1502;  
 CC (1)  
 CC SEQUENCE FROM N.A.  
 RP STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shintzu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,  
 RA Shida T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- CATALYTIC ACTIVITY: D-mannonate = 2-dehydro-3-deoxy-D-glucuronate +  
 CC H(2)O.  
 CC -1- PATHWAY: Glucuronate pathway.  
 CC -1- SIMILARITY: Belongs to the mannate dehydratase family.  
 CC -----  
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 CC -----  
 CC EMBL: AP003185; BAB79857.1; -  
 CC DR HAMAP: MF\_00106; -; 1.  
 CC DR InterPro: IPR004628; Man\_dehyd.  
 CC DR Pfam: PF03786; UXUA; 1.  
 CC DR TIGRFAMs: TIGR00695; uxua; 1.  
 CC KW Lyase; Complete proteome.  
 CC SQ SEQUENCE 350 AA; 40293 MW; 80FB0F9CFED78A0B CRC64;  
 CC  
 CC Query Match 0.5%; Score 7; DB 1; Length 350;  
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 72  
 ID UXUA\_CLOPE STANDARD; PRT; 350 AA.  
 AC Q8XP15;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

RESULT 73  
 ID HIS8\_STAM STANDARD; PRT; 352 AA.  
 AC Q99VD9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-  
 DE phosphate transaminase).  
 GN HIS8 OR SAV0724 OR SA0679.  
 OS Staphylococcus aureus (strain Mu50 / ATCC 700639), and  
 OS Staphylococcus aureus (strain N315).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 CC NCB1\_TaxID=158878; 158879;  
 CC (1)  
 CC SEQUENCE FROM N.A.  
 RP STRAIN=Mu50 / ATCC 700639, and N315;  
 RX MEDLINE=21311952; PubMed=11418146;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iken J.-Q., Ito T.,  
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Inoue R.-I., Kaio C.,  
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
 RA Hattori M., Ogasawara N., Hayashi H., Hiratsuku K.;  
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
 aureus.";

RL Lancel 357:1225-1240(2001).  
 CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-  
 CC (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.  
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -1- PATHWAY: Histidine biosynthesis; seventh step.  
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, AP003360; BAB5686.1; -  
 DR EMBL, AP003131; BAB41912.1; -  
 DR PIR, B99844; B99844.  
 DR HAMAP, MF\_01023; -; 1.  
 DR InterPro, IPR004839; AminoTransferase/2.  
 DR InterPro, IPR005861; HisP aminoTrans.  
 DR Pfam, PF00155; aminoTran\_1\_2; 1.  
 DR TIGRfam, TIGR01141; hisC\_1.  
 DR PROSITE, PS00599; AA TRANSFER CLASS\_2; 1.  
 DR Histidine biosynthesis; Transferase; AminoTransferase;  
 DR Pyridoxal phosphate; Complete proteome.  
 FT BINDING 221 221  
 FT SEQUENCE 352 AA; 39788 MW; D6AA6041524D4700 CRC64;  
 SQ  
 Query Match 0.5%; Score 7; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 ILFGAGL 109  
 Db 83 ILFGAGL 89  
 RESULT 74  
 HIS8\_STAAW STANDARD; PRT; 352 AA.  
 ID HIS8\_STAAW  
 AC Q8NNK3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole aceto-  
 DE phosphate transaminase).  
 GN HIS8 OR MM0686.  
 OS Staphylococcus aureus (strain MW2).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=196620;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22040717; PubMed=12044378;  
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hiramoto K.,  
 RT "Genome and virulence determinants of high virulence community-  
 RT acquired MRSA".  
 RL Lancel 359:1819-1827(2002).  
 CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-  
 CC (imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.  
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -1- PATHWAY: Histidine biosynthesis; seventh step.  
 CC -1- SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, AP004824; BAB94551.1; -  
 DR HAMAP, MF\_01023; -; 1.  
 DR InterPro, IPR001176; ACC synthase.  
 DR InterPro, IPR004839; AminoTransferase/2.  
 DR InterPro, IPR005861; HisP aminoTrans.  
 DR Pfam, PF00155; aminoTran\_1\_2; 1.  
 DR PRINTS, PR00753; ACCSYNTHASE.  
 DR TIGRfam, TIGR01141; hisC\_1.  
 DR PROSITE, PS00599; AA TRANSFER CLASS\_2; 1.  
 DR Histidine biosynthesis; Transferase; AminoTransferase;  
 DR Pyridoxal phosphate; Complete proteome.  
 FT BINDING 221 221  
 FT SEQUENCE 352 AA; 39846 MW; D6ACC297E67C744 CRC64;  
 SQ  
 Query Match 0.5%; Score 7; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 ILFGAGL 109  
 Db 83 ILFGAGL 89  
 RESULT 75  
 TGDS\_MOUSE  
 ID TGDS\_MOUSE  
 AC Q8VDR7;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE dTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46).  
 GN TGDS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Tashiro S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,  
 RA Bosak S.A., Mesman P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,  
 RA Villalon D.K., Mizzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Rahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 CC -1- CATALYTIC ACTIVITY: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-  
 CC glucose + H(2)O.  
 CC -1- COFACTOR: NAD (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTPD-GLUCOSE  
 CC DEHYDRATASE SUBFAMILY.  
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CC -----  
DR EMBL; BC021419; AAH21419.1; -  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
KW lyase; NAD.  
SQ SEQUENCE 355 AA; 40598 MW; ABA1913359C266FB CRC64;

Query Match 0.5%; Score 7; DB 1; Length 355;  
Best Local Similarity 100.0%; Pred.No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VOLAKEL 38  
|||  
Db 266 VOLAKEL 272

Search completed: December 18, 2003, 09:12:29  
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 ; Search time 32 Seconds  
(without alignments)  
4216.396 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403  
Sequence: 1 MATOQKASDERISQFDHNL.....SKYLTLQKWLFPSPFIQK 1403

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

1: PIR\_76: \*  
2: pirl: \*  
3: pirl: \*  
4: pirl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	946	67.4	1232	2	A55478 neuronal apoptosis
2	35	2.5	1447	2	T42628 ABC transporter, A
3	9	0.6	210	2	E95198 hypothetical prote
4	9	0.6	414	2	T50010 probable transcrip
5	8	0.6	827	2	H83217 V-ATPase proteolip
6	6	0.6	120	2	T44670 hypothetical prote
7	8	0.6	146	2	F72595 hypothetical prote
8	8	0.6	147	2	H75319 hypothetical prote
9	8	0.6	152	2	C69546 apoptosis inhibito
10	8	0.6	155	2	T30489 transcription term
11	8	0.6	156	2	J70658 membrane protein c
12	8	0.6	219	2	UC5484 membrane protein c
13	8	0.6	219	2	AP2906 membrane protein c
14	8	0.6	219	2	G97681 membrane protein c
15	8	0.6	230	2	AB0553 daunorubicin biosy
16	8	0.6	272	2	A43306 glycosyl transfera
17	8	0.6	290	2	H64431 hypothetical prote
18	8	0.6	324	2	C41608 hypothetical prote
19	8	0.6	329	2	T27793 proteinase IV homo
20	8	0.6	335	2	E69990 probable transpo
21	8	0.6	345	2	C71237 hypothetical prote
22	8	0.6	358	2	T01902 probable transpo
23	8	0.6	365	2	A97163 probable transpo
24	8	0.6	391	2	T34831 acyl-coa dehydrog
25	8	0.6	396	1	A58938 surface protein in
26	8	0.6	422	2	F75151 hypothetical prote
27	8	0.6	425	2	H71167 probable S-adenosy
28	8	0.6	489	2	F65125 probable general s
29	8	0.6	548	1	A26511 amds protein - Eme

30	8	0.6	824	2	B47301 ViB4 homolog - Bo
31	8	0.6	845	2	T12537 hypothetical prote
32	8	0.6	934	2	T03742 probable ligand-ga
33	8	0.6	1026	2	T03179 probable DNA-direc
34	8	0.6	1188	2	UC4889 phosphatidylinosit
35	8	0.6	1189	2	UC6118 SH2-containing ino
36	8	0.6	1239	2	S74355 hypothetical prote
37	8	0.6	1280	2	T00365 hypothetical prote
38	8	0.6	1360	2	F96596 hypothetical prote
39	8	0.6	1537	2	F66509 CT147 hypothetical
40	8	0.6	1537	2	C81558 conserved hypothet
41	8	0.6	1537	2	H72112 ct147 hypothetical
42	8	0.5	45	2	AC0724 hypothetical prote
43	8	0.5	66	2	AP2722 hypothetical prote
44	8	0.5	72	2	C97504 hypothetical prote
45	8	0.5	87	2	T50006 hypothetical prote
46	8	0.5	88	2	A13122 hypothetical prote
47	8	0.5	88	2	F98164 insertion element
48	8	0.5	89	2	T35348 probable membrane
49	8	0.5	90	2	B42523 A54L protein - Vac
50	8	0.5	97	2	T35051 hypothetical prote
51	8	0.5	103	2	A39980 TyA protein - Yeas
52	8	0.5	103	2	C69034 conserved hypothet
53	8	0.5	106	2	F71681 hypothetical prote
54	8	0.5	113	2	A85639 hypothetical prote
55	8	0.5	121	2	T49201 Yippee-like protei
56	8	0.5	125	2	H81997 probable lipoprote
57	8	0.5	125	2	F81226 lipoprotein, proba
58	8	0.5	130	2	A82599 conserved hypothet
59	8	0.5	130	2	G75175 hypothetical prote
60	8	0.5	134	2	C65115 hypothetical 15.2
61	8	0.5	134	2	B91142 hypothetical prote
62	8	0.5	134	2	B85987 hypothetical prote
63	8	0.5	137	2	T42327 hypothetical prote
64	8	0.5	140	2	C70223 conserved hypothet
65	8	0.5	145	2	B83611 conserved hypothet
66	8	0.5	149	2	C95319 conserved hypothet
67	8	0.5	152	2	B89947 hypothetical prote
68	8	0.5	155	2	S38662 interlukin-2 - go
69	8	0.5	158	2	H75028 probable H+-transp
70	8	0.5	162	2	D71214 dihydrofolate redu
71	8	0.5	165	2	G82322 hypothetical prote
72	8	0.5	175	2	S73337 hypothetical prote
73	8	0.5	175	2	S69636 hypothetical prote
74	8	0.5	179	2	T49816 hypothetical prote
75	8	0.5	189	2	B49845 uncharacterized pr
76	8	0.5	192	2	C97315 hypothetical prote
77	8	0.5	192	2	A83587 hypothetical prote
78	8	0.5	194	2	G71038 hypothetical prote
79	8	0.5	196	2	B49453 transcription init
80	8	0.5	207	2	G75118 processome, chain
81	8	0.5	216	2	A37762 hypothetical prote
82	8	0.5	221	2	A99970 hypothetical prote
83	8	0.5	223	2	H83359 DC1 protein precu
84	8	0.5	224	2	S71749 hypothetical prote
85	8	0.5	225	2	C84376 hypothetical prote
86	8	0.5	227	2	A48412 hypothetical prote
87	8	0.5	230	2	S71747 DAG protein precu
88	8	0.5	231	2	G83883 L-ribulose-5-phosp
89	8	0.5	232	2	T09003 response regulato
90	8	0.5	232	2	A27503 testis-specific pr
91	8	0.5	234	2	T30427 probable apopto
92	8	0.5	237	2	H90492 ABC transporter, A
93	8	0.5	243	2	AG2169 carbonate dehydrat
94	8	0.5	247	2	C71229 hypothetical prote
95	8	0.5	248	2	G75196 hypothetical prote
96	8	0.5	251	2	C97789 hypothetical prote
97	8	0.5	252	2	F97949 hypothetical prote
98	8	0.5	252	2	B95082 amino acid ABC tra
99	8	0.5	253	2	C72758 probable enoyl-CoA
100	8	0.5	254	2	C72622 hypothetical prote

## ALIGNMENTS

## RESULT 1

A55478  
neutroal apoptosis inhibitory protein - human  
N:Alternate names: NAIP  
C:Species: Homo sapiens (man)  
C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 02-Feb-2001  
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuclet, G.; Yaregbi, Z.; Farhani, R.; Baird, S.  
Cell 80, 167-178, 1995  
A>Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi  
A:Reference number: A55478; MIM:95112344; PMID:7613013  
A:Molecule type: mRNA  
A:Residues: 1-1232 <ROY>  
A:Cross-references: GB:U19251  
C:Gene: GDB:SMA6; SMA  
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300  
A:Map position: 5q12.2-5q13  
C:Keywords: apoptosis; APP; glycoprotein; nucleotide binding; P-loop; transmembrane prot  
F:470-477/Region: nucleotide-binding motif A (P-loop)  
F:479-496/Domain: transmembrane #status predicted <TM1>  
F:476/Binding site: ATP (Lys) #status predicted <TM2>  
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 67.4%; Score 946; DB 2; Length 1232;  
Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MATQQAASPERISOPDNLPLPSALLGLDAVOLAKELSEEEKKAKKQKYNQMRSE	60
DB	1	MATQQAASPERISOPDNLPLPSALLGLDAVOLAKELSEEEKKAKKQKYNQMRSE	60
QY	61	AKRLTPTTYEPYSSWIPQEWMAAGFTGVKSGICFCFCSILPFGAGITLPIEDHKRF	120
DB	61	AKRLTPTTYEPYSSWIPQEWMAAGFTGVKSGICFCFCSILPFGAGITLPIEDHKRF	120
QY	121	HPDCGFLNKGVDGNIAYDRIYKRLKSLRGSKMYOESEARLASFNNMPTVQGISPCV	180
DB	121	HPDCGFLNKGVDGNIAYDRIYKRLKSLRGSKMYOESEARLASFNNMPTVQGISPCV	180
QY	181	LSEAGFVFGKQDPTVCCFCGCGCLGNWBERGDDPMKEHAKMPKCEFLRSKSSSEITQYI	240
DB	181	LSEAGFVFGKQDPTVCCFCGCGCLGNWBERGDDPMKEHAKMPKCEFLRSKSSSEITQYI	240
QY	241	QSYKGVDTTGEHFNVMWVORELPMASAYCNDISFAVEELRLDSFCDMPRESAVGVALA	300
DB	241	QSYKGVDTTGEHFNVMWVORELPMASAYCNDISFAVEELRLDSFCDMPRESAVGVALA	300
QY	301	KAGLFTYTGKIDVOFCGCGCLGNWBERGDDPLDHTRCPCNPONKSSAEVTPDLOS	360
DB	301	KAGLFTYTGKIDVOFCGCGCLGNWBERGDDPLDHTRCPCNPONKSSAEVTPDLOS	360
QY	361	RGEICELLETTSESNLEDSIAGVPIVEMAOGEAOWFOGAKNLEQLAAATTSAPFHM	420
DB	361	RGEICELLETTSESNLEDSIAGVPIVEMAOGEAOWFOGAKNLEQLAAATTSAPFHM	420
QY	421	LLDISSLATDHLGCDLSIASKHISKPYQEPVLVPEVGNLNSVMCEGASGTVLL	480
DB	421	LLDISSLATDHLGCDLSIASKHISKPYQEPVLVPEVGNLNSVMCEGASGTVLL	480
QY	481	KKIAFLMASCCEPLNRFQVLYSLSTRDEGLASIDOLLEKSGVTECKRNIIQ	540
DB	481	KKIAFLMASCCEPLNRFQVLYSLSTRDEGLASIDOLLEKSGVTECKRNIIQ	540
QY	541	QAKNOVLFLLDYKICSIPOVIGKLIQKHLSTCLLAVRTNRARDIRRYLLEITL	600
DB	541	QAKNOVLFLLDYKICSIPOVIGKLIQKHLSTCLLAVRTNRARDIRRYLLEITL	600

QY	601	AFPPYNTVCTLRKLFESHNMTRLRKFMVYFGKKNOSLOKIQTPLEVAALICAMRFQYFDP	660
DB	601	AFPPYNTVCTLRKLFESHNMTRLRKFMVYFGKKNOSLOKIQTPLEVAALICAMRFQYFDP	660
QY	661	FDVAVAFKSYMERLSLRNKAATIELIKATVSSCGELAKGFFSCCFEPPNDLAEAGVBD	720
DB	661	FDVAVAFKSYMERLSLRNKAATIELIKATVSSCGELAKGFFSCCFEPPNDLAEAGVBD	720
QY	721	EDLTCLMSKFTQARLRFPRFLSPAFQFELAGRLIEILDSDROHOLGTYHLKOINS	780
DB	721	EDLTCLMSKFTQARLRFPRFLSPAFQFELAGRLIEILDSDROHOLGTYHLKOINS	780
QY	781	PMWTASANNFLNVTSSLPSTKAGPKIVSHLHLVDNKSLENISENDYLKQPEISLO	840
DB	781	PMWTASANNFLNVTSSLPSTKAGPKIVSHLHLVDNKSLENISENDYLKQPEISLO	840
QY	841	MQLRLGLMOICPOAFYSMTSEHLVLALKTAVQSNVTVAACSPFLQFLOGRITLTALNL	900
DB	841	MQLRLGLMOICPOAFYSMTSEHLVLALKTAVQSNVTVAACSPFLQFLOGRITLTALNL	900
QY	901	QYFFDHPESLSLRSHFPIRGNKTSPPRAHFSVLETCEFSQVPTTIDQYASAFEPNEM	960
DB	901	QYFFDHPESLSLRSHFPIRGNKTSPPRAHFSVLETCEFSQVPTTIDQYASAFEPNEM	960
QY	961	ERVLAKEDNVKSYNDMORRASPDLSTGYMKLSPKQYKIPCLEVDVNDIDVVGDMLEIL	1020
DB	961	ERVLAKEDNVKSYNDMORRASPDLSTGYMKLSPKQYKIPCLEVDVNDIDVVGDMLEIL	1020
QY	1021	MTVFSASORIELHNSRGFTESIRPALISKASVYTKSISKLELSAAEQELTLTSLR	1080
DB	1021	MTVFSASORIELHNSRGFTESIRPALISKASVYTKSISKLELSAAEQELTLTSLR	1080
QY	1081	SLVSGTIOGDDIPLNLDKFLCKELSYDLSEGNINVSIVPEEPFNHNEKLLQISA	1140
DB	1081	SLVSGTIOGDDIPLNLDKFLCKELSYDLSEGNINVSIVPEEPFNHNEKLLQISA	1140
QY	1141	EYDPSKLV 1148	
DB	1141	EYDPSKLV 1148	

## RESULT 2

742628  
neutroal apoptosis inhibitory protein 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
R:Yaregbi, Z.; Dies, E.; Gros, P.; Mackenzie, A.  
Mamm. Genome 10, 761-763, 1999  
A>Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for mur  
A:Accession: T42628  
A:Reference number: 222179; MIM:9315342; PMID:10384056  
A:Staeus: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1447 <YAB>  
A:Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC73002.1  
C:Gene: Naip2

Query Match 2.5%; Score 35; DB 2; Length 1447;  
Best Local Similarity 100.0%; Pred. No. 26-26;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	193	DTVQCFSGCGCLGNWBERGDDPMKEHAKMPKCEFL	227
DB	193	DTVQCFSGCGCLGNWBERGDDPMKEHAKMPKCEFL	227

## RESULT 3

E95198  
ABC transporter, ATP-binding protein SPI704 [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae



C/Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 11-Jan-2002  
 C/Accession: E95198  
 R/Petterlin, H.; Nelson, K.E.; Paulsen, I.T.; Risen, J.A.; Read, T.D.; Peterson, S.; Heid  
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holzapfel,  
 neon, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001  
 A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
 A./Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.  
 A/Reference number: A95000; PMID:21357209; PMID:11463916  
 A/Accession: E95198  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-210 <KUR>  
 A/Cross-references: GB:AE005672; PIDN:AAK75782.1; PID:g14973198; GSPDB:GN00164; TIGR:SP4  
 A/Experimental source: strain TIGR4  
 C/Genetics: SBI704  
 A/Gene: SBI704  
 C/Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 0.6%; Score 9; DB 2; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 GSGKTVLLK 481  
 DB 38 GSGKTVLLK 46

RESULT 4  
 T50010  
 hypothetical protein T31P16.50 - *Arabidopsis thaliana*  
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 C/Accession: T50010  
 R/Sevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wöhlmann, P.; Sm  
 submitted to the Protein Sequence Database, May 2000  
 A/Reference number: Z25027  
 A/Accession: T50010  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-414 <BEV>  
 A/Cross-references: EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.50  
 A/Experimental source: cultivar Columbia; BAC clone T31P16  
 C/Genetics:  
 A/Gene: ATSP:T31P16.50  
 A/Map position: 5  
 A/Introns: 55/3; 107/3; 161/1; 207/3; 219/3

Query Match 0.6%; Score 9; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 LAKELEEE 42  
 DB 168 LAKELEEE 176

RESULT 5  
 H83217  
 probable transcription regulator PA3420 [imported] - *Pseudomonas aeruginosa* (strain PA01  
 C/Species: *Pseudomonas aeruginosa*  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: H83217  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; Br  
 adman, S.; Olson, Y.; Brody, L.U.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
 ; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A/Reference number: A82950; PMID:20437337; PMID:10984043  
 A/Accession: H83217  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-827 <STO>

A/Cross-references: GB:AE004763; GB:AE004091; NID:g9949556; PIDN:AA06808.1; GSPDB:GN001  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: PA3420

Query Match 0.6%; Score 9; DB 2; Length 827;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 AGSGKTVLL 480  
 DB 42 AGSGKTVLL 50

RESULT 6  
 T44670  
 V-ATPase proteolipid [imported] - *Desulfurococcus* sp. (strain SY) (fragment)  
 C/Species: *Desulfurococcus* sp.  
 A/Variety: strain SY  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Sep-2000  
 C/Accession: T44670  
 R/Shibui, H.; Hamamoto, T.; Yohda, M.; Kagawa, Y.  
 Biochem. Biophys. Res. Commun. 234, 341-345, 1997  
 A/Title: The stabilizing residues and the functional domains in the hyperthermophilic V-  
 A/Reference number: JCS532; PMID:97320421; PMID:9177272  
 A/Accession: T44670  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-120 <SHI>  
 A/Cross-references: EMBL:U96487; PIDN:AA64412.1  
 A/Experimental source: strain SY  
 C/Superfamily: Na<sup>+</sup>-ATPase complex X chain

Query Match 0.6%; Score 8; DB 2; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 ILFGAGLT 110  
 DB 61 ILFGAGLT 68

RESULT 7  
 F72695  
 hypothetical protein APE0982 - *Aeropyrum pernix* (strain K1)  
 C/Species: *Aeropyrum pernix*  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C/Accession: F72695  
 R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
 DNA Res. 6, 83-101, 1999  
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr  
 A/Reference number: A72450; PMID:99310339; PMID:10382966*

Query Match 0.6%; Score 8; DB 2; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 LSLSTRP 511  
 DB 36 LSLSTRP 43

RESULT 8  
 H75319

hypothetical protein - *Deinococcus radiodurans* (strain R1)  
 C/Species: *Deinococcus radiodurans*  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C/Accession: H75319  
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mc  
 Science 286, 1571-1577, 1999  
 A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
 A/Reference number: A75250; MUID:20036896; PMID:10567266  
 A/Accession: H75319  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-147 <WHI>  
 A/Cross-references: GB:AE002042; GB:AE00513; NID:96459848; PIDN:AAF11610.1; PID:9645985  
 C/Genetics:  
 A/Genetic: DR2056  
 A/Map position: 1

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 147;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 888 LOGRTLT 695  
 Db 109 LOGRTLT 116

RESULT 9  
 hypothetical protein AF2371 - *Archaeoglobus fulgidus*  
 C/Species: *Archaeoglobus fulgidus*  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
 C/Accession: C69546  
 R/Kienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 Nature 390, 364-370, 1997  
 A/Author: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A/Reference number: A69250; MUID:98049343; PMID:9389475  
 A/Accession: C69546  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-152 <KLE>  
 A/Cross-references: GB:AE001112; GB:AE00782; NID:92689435; PIDN:AAB91296.1; PID:9265072

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 152;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1196 VPFVASLP 1203  
 Db 95 VPFVASLP 102

RESULT 10  
 T10489  
 Apoptosis inhibitor - *Lymantria dispar* nuclear polyhedrosis virus  
 C/Species: *Lymantria dispar* nuclear polyhedrosis virus, LdNPV  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C/Accession: J30489  
 R/Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Roh  
 Virology 253, 17-34, 1999  
 A/Title: Sequence and analysis of the genome of a baculovirus pathogenic for *Lymantria d*  
 A/Reference number: J20836; MUID:99124785; PMID:9887315  
 A/Accession: J30489  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-155 <KUZ>  
 A/Cross-references: EMBL:AF081810; PIDN:AACT0325.1

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 155;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 162 RLSPFNW 169  
 Db 7 RLSPFNW 14

RESULT 11  
 A70658  
 transcription termination factor nusB [similarity] - *Mycobacterium tuberculosis* (strain  
 N/Alternate names: N utilization substance protein B  
 C/Species: *Mycobacterium tuberculosis*  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C/Accession: A70658  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
 i Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A/Author: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
 A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genom  
 A/Reference number: A70500; MUID:98295987; PMID:9634220  
 A/Accession: A70658  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-156 <COL>  
 A/Cross-references: GB:Z83863; GB:AL123456; NID:93261685; PIDN:CAB06175.1; PID:91781069  
 A/Experimental source: strain H37Rv  
 C/Genetics:  
 A/Genetic: nusB  
 C/Superfamily: nusB protein  
 C/Keywords: transcription termination

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 156;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 31 AVOLAKEL 38  
 Db 115 AVOLAKEL 122

RESULT 12  
 JCS484  
 membrane protein ccmb - *Rhizobium etli*  
 C/Species: *Rhizobium etli*  
 C/Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 20-Aug-1999  
 C/Accession: JCS484  
 R/Aguiar, G.R.; Soberon, M.  
 Gene 182, 129-135, 1996  
 A/Title: Cloning and sequence analysis of the *Rhizobium etli* ccmb and ccmb genes involv  
 A/Reference number: JCS483; MUID:97136701; PMID:8982078  
 A/Accession: JCS484  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-219 <AGU>  
 A/Cross-references: GB:U52866; NID:91279856; PIDN:AAB40906.1; PID:91279859  
 C/Comment: This protein has six transmembrane regions.  
 A/Genetics:  
 C/Superfamily: cytochrome c biogenesis protein CycW

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 219;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 23 LSALGLD 30  
 Db 58 LSALGLD 65

RESULT 13  
AF2906  
Hypothetical protein ccmB [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AF2906  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guehner, D.; Kutayvan, T.; Levy, R.; Li, M.; Mclell  
/ Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
Bret, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF2906  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <KUR>  
A:Cross-references: GB:AE008688; PIDN:AAI43668.1; PID:g17741193; GSPDB:GN00186  
A:Experimental source: strain C58 (Dupont)  
A:Genetics:  
A:Gene: ccmB  
A:Map position: circular chromosome  
C:Superfamily: cytochrome c biogenesis protein CycW  
Query Match 0.6%; Score 8; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 23 LSALIGLD 30  
DB 58 LSALIGLD 65  
RESULT 14  
G97681  
membrane protein ccmB [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: G97681  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman,  
A.; Liu, F.; Wolim, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: G97681  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-219 <KUR>  
A:Cross-references: GB:AE007669; PIDN:AAK88408.1; PID:g15157901; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_4870  
A:Map position: circular chromosome  
C:Superfamily: cytochrome c biogenesis protein CycW  
Query Match 0.6%; Score 8; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 23 LSALIGLD 30  
DB 58 LSALIGLD 65  
RESULT 15  
AB0553  
Probable deox-family transcription regulator STY0448 [imported] - Salmonella enterica su  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AB0553  
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AB0553  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-230 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD08866.1; PID:g16501679; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY0448  
Query Match 0.6%; Score 8; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 468 VEGASG 475  
DB 51 VEGASG 58  
RESULT 16  
AA3306  
daunorubicin biosynthesis regulatory protein dnri [imported] - Streptomyces peucetius  
C:Species: Streptomyces peucetius  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: AA3306  
R:Stutzman-Bigwall, K.J.; Otten, S.L.; Hutchinson, C.R.  
J. Bacteriol. 174, 144-154, 1992  
A:Title: Regulation of secondary metabolism in Streptomyces spp. and overproduction of d  
A:Reference number: AA3306; MUID:92104954; PMID:1729206  
A:Accession: AA3306  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <STU>  
A:Cross-references: GB:M60237; NID:g153242; PIDN:AAA26736.1; PID:g153243  
A:Experimental source: ATCC 29050  
A:Note: sequence extracted from NCBI backbone (NCBIN:75271, NCBI:75272)  
C:Keywords: transcription regulation  
Query Match 0.6%; Score 8; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 19 LIPERLAL 26  
DB 185 LIPERLAL 192  
RESULT 17  
H64431  
glycosyl transferase (EC 2.4.-.-) - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 06-Jan-2003  
C:Accession: H64431  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
; Reith, C.L.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodex, A.;  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.  
A:Reference number: A64300; MUID:96337999; PMID:8686087  
A:Accession: H64431  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Cross-references: GB:U67549; GB:L77117; NID:g1591709; PID:g1592318; TIGR:WJ057; PID:g1  
A:Map position: FOR96513-997385  
C:Superfamily: Neisseria meningitidis glycosyl transferase A  
C:Keywords: glycosyltransferase

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465
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hypothetical protein 3 (hima\_5' region) - Rhodobacter capsulatus  
C:Species: Rhodobacter capsulatus  
C:Date: 10-Jul-1992 #hemmoa 2001-1

C:\Accession: C41608 "sequence\_revision 10-Jul-1992 #text\_change 18-Jun-1999  
 R:\Toussaint, B.; Boec, C.; Richard, P.; Colbeau, A.; Vignais, P.M.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 10749-10753, 1991  
 A>Title: A mutation in a Rhodospirillum rubrum capsulatus gene encoding an integration host factor  
 A:Reference number: A41608; PMID:92073365; PMID:1961742  
 A:Accession: C41608  
 A:Strain: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-324 <TOU>  
 A:Cross-references: GB:M84030; NID:g151940; PIDN:AAA26127.1. Pro. 577003  
 C:\Spectrum: 3'-oxoacyl-[acyl-carrier]-protein

Query Match	0.64	Score 8	DB 2	Length 324
Best Local Similarity	100.0%	Pred. No. 25		
Matches	8	Conservative	0	Mismatches
QY	297	AALAAAGL	304	Indels
				Gaps
DB	233	AALAAAGL	240	

hypothetical protein ZK228.7 - *Caenorhabditis elegans*  
12/1/93  
C/Species: *Caenorhabditis elegans*  
Date: 15 Oct 1993

C:\Accession: 15-Oct-1999 #sequence\_rev\15Oct-1999 #text\_change 21-Jun-2000  
R:\Baehren, V.  
submitted to the EMBL Data Library, November 1996  
A:\Accession: T27793  
A:\Status: preliminary; translated from GB/EMBL/DDAT  
A:\Residue type: DNA  
A:\Cross-references: EMBL:Z82086; PIDN:CAB0498.1; GSTDB:GN00023; CESP:ZK228.7  
C:\Genetics:  
A:\Gene: CESP:ZK228.7  
A:\Map position: 5  
A:\Intons: 107/1; 168/3; 270/1  
A:\Superfamily: Ctenocephalid

Query Match 0.6%; Score 8; DB 2; Length 329  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0.0; Mismatch 0.0

QY	1072	LLLLLPSTL	1079	0	Anders	0	Gaps	0
Db	249	LLLLLPSTL	256					

proteinase IV homolog yteI - *Bacillus subtilis*  
C:Species: *Bacillus subtilis*  
Date: 07/20/2011

Citation: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C\_Accession: E69990  
R\_Kunst, P.; Ogaewara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux  
C.; Bron, S.; Brouillet, S.; Bruecht, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chid

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 390, 249-256, 1997

leech, J., Harwood, U., Fritz, C., Fujita, M., Fujita, Y., Puma, S., Gallizzi, A., Gallier, A., Koetter, P., Koningsstein, G., Krogsh, S., Kumano, S., Holsappel, S., Hulio, M. P. Y., M., Ogawa, K., Ogawa, A., Oudga, B., Park, S.M., Levine, A., Liu, H., Masuda, A., Lardinois, R., Rieger, M., Rijola, C., Rooha, A., Roche, B., Rose, M., Sadate, V., Poh, T.M., Portetelle, A., Authors: Schlicht, S., Schroeder, R., Scoffone, T., Terresta, P., Sekiguchi, J., Sato, T., Scanlon, T., Munters, P., Mpat, A., Tanaka, T., Terepta, P., Tokimoto, A., Tosato, V., Uchiyama, A., Authors: Yoshikawa, H. F., Zunaeto, E., Yamane, K., Yaguchi, K., Yata, K., Yoshida, A., Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A Reference number: A69580; PMID:98044033; PMID:9384377  
A.Accession: E6990  
A.Strains: pE1111; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-335 <KUN>  
A.CROSB-References: GB:299119; GB:AU009126; NID:52635411; PIDN:CAB14931.1; PID:g2635437  
A.Exposed-References: GB:299119; NID:52635411; PIDN:CAB14931.1; PID:g2635437  
C.Genetics: 168  
A.Gene: yte1

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      1 match.      0.6%; Score 8; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 25;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
QY      1082 LEVSGTQ 1089
      |||||
Db      63 LEVSGTQ 70

```

probable transport-ATP binding protein - *Pyrococcus horikoshii*  
C/Species: *Pyrococcus horikoshii*  
/Date: 14-Aug-1999 #-----

C/Accession: F01336 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
 R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekino,  
 M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
 DNA Res. 5, 55-76, 1998  
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon  
 A/Accession: F01337  
 A/Reference number: A71000, PMID:98344137, PMID:9679194  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-345 <RAW>  
 A/Cross-references: GR:A000001, NID:G3236128, PID:BAA2226.1, PID:G3256543  
 A/Experimental source: strain OT3  
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 A/Genetic: :  
 A/Genes: PH0157  
 C/Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C/Keywords: ATP  
 F/16-207/Domain: ATP-binding cassette domain

Query Match

Best Local Similarity	0.6%	Score 8	DB 2	Length 345
Matches	8	Conservative	0	Mismatches
CY	473	GGGKTVLL	480	Indels
				Gaps
Db	36	GGGKTVLL	43	

hypothetical protein T12H20.10 - *Arabidopsis thaliana*  
C1Species: *Arabidopsis thaliana* (mouse-ear cress)  
Date: 05-11-2005

C/Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 30-Sep-2002  
 C/Accession: T01992  
 R/Cotton, M.; Graves, T.; Sutherer, C.; Modde, T.  
 submitted to the EMBL Data Library, July 1998

A>Description: The sequence of A. thaliana T12H20.  
A:Reference number: Z14453  
A:Accession: T01902  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-358 <COT>  
A:Cross-references: EMBL:AF080119; NID:G3600029; PID:G3600031  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Map position: 4  
A:Note: T12H20.10  
C:Superfamily: 2,4-dihydroxyhept-2-ene-1,7

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 358;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LKSRURGG 152  
DB 80 LKSRURGG 87

RESULT 23  
A:7163  
Probable GTPase, YVAF B. subtilis ortholog [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: A97163  
R:NoUnlabeled, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10  
A:Reference number: A96900; MWID:21359325; PMID:21359325  
A:Accession: A97163  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80092.1; PID:G15025125; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2134  
C:Superfamily: Yeast probable purine nucleotide-binding protein YBR025C

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 365;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LREERQKE 45  
DB 249 LREERQKE 256

RESULT 24  
T34831  
acyl-coa dehydrogenase redw - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 21-Jan-2000  
C:Accession: T34831  
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z21558  
A:Accession: T34831  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-391 <DLI>  
A:Cross-references: EMBL:AL021530; PIDN:CAA16488.1; GSPDB:GN00070; SCOEDB:SC2E9.20  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: redw, SCOEDB:SC2E9.20  
C:Superfamily: acyl-CoA dehydrogenase

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 391;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LGIDAVOL 34  
DB 334 LGIDAVOL 341

RESULT 25  
A58938  
surface protein rhoptry ROP1 precursor - Toxoplasma gondii  
C:Species: Toxoplasma gondii  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A58938; A45644; S37697  
R:Boothroyd, J.C.  
submitted to GenBank, July 1995  
A:Reference number: A58938  
A:Accession: A58938  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-396 <BOO>  
A:Cross-references: GB:M71274; NID:9897822; PIDN:AAA69859.1; PID:9897823  
A:Note: revision to sequence reported in A45644  
R:Boothroyd, J.C.; Schwartzman, J.D.; Boothroyd, J.C.  
Mol. Biochem. Parasitol. 50, 1-15, 1992  
A:Title: A Toxoplasma gondii rhoptry protein associated with host cell penetration has w  
A:Reference number: A45644; MWID:92178277; PMID:1542304  
A:Accession: A45644  
A:Molecule type: mRNA  
A:Residues: 'MACRQLCSQNLFFPLRDYCTDPT', 1-352, 'FPQR', 358-364, 'R', 366, 'I', 393, 'SP', 396,  
A:Cross-references: EMBL:M71274; NID:9897822  
A:Note: sequence extracted from NCBI backbone (NCBIN:85178, NCBI:85179)  
C:Superfamily: surface protein rhoptry  
C:Keywords: surface antigen  
P:1-21/Domain: signal sequence #status predicted <SIG>  
P:22-396/Product: surface protein rhoptry #status predicted <MAT>

Query Match  
Best Local Similarity 100.0%; Score 8; DB 1; Length 396;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
DB 363 FGAGLTRL 370

RESULT 26  
F75151  
hypothetical protein PAB0247 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: F75151  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A>Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc  
A:Reference number: A75001  
A:Accession: F75151  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-422 <NAN>  
A:Cross-references: GB:AJ48284; GB:AL096836; NID:G5457730; PIDN:CAB49293.1; PID:G545780;  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB0247  
C:Superfamily: conserved hypothetical protein MJ1095

Query Match  
Best Local Similarity 100.0%; Score 8; DB 2; Length 422;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1353 LPRILRLN 1360  
DB 38 LPRILRLN 45

## RESULT 27

H71167  
 Probable S-adenosyl-L-homocysteine hydrolase - *Pyrococcus horikoshii*  
 C/Species: *Pyrococcus horikoshii*  
 C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
 C/Accession: H71167  
 R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit  
 DNA Res. 5, 55-76, 1998  
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A/Reference number: A71000; MUID:98344137; PMID:9679194  
 A/Accession: H71167  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-425 <RAW>  
 A/Cross-references: GB:AP000002; NID:G3236129; PIDN:BAA29629.1; PID:G3256946  
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C/Genetics:  
 A/Genes: PH0540  
 C/Superfamily: adenosylhomocysteinease

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 425;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 296 VAALAKAG 303  
 DB 93 VAALAKAG 100

## RESULT 28

F65125  
 Probable general secretion pathway protein b - *Escherichia coli* (strain K-12)  
 C/Species: *Escherichia coli*  
 C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C/Accession: F65125  
 R/Balster, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 Science 277, 1453-1462, 1997  
 A/Title: The complete genome sequence of *Escherichia coli* K-12.  
 A/Reference number: A64720; MUID:97426617; PMID:9278503  
 A/Accession: F65125  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-489 <BLAT>  
 A/Cross-references: GB:AE000409; GB:U00096; NID:G1789718; PIDN:AACT6348.1; PID:G1789720;  
 A/Experimental source: strain K-12, substrain MG1655  
 C/Genetics:  
 A/Genes: yheD

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 489;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 470 GAGSGGKT 477  
 DB 26 GAGSGGKT 33

## RESULT 29

A26511  
 amds protein - *Emeticella nidulans*  
 C/Species: *Emeticella nidulans*, *Aspergillus nidulans*  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Sep-1999  
 C/Accession: A26511  
 R/Corrick, C.M.; Twomey, A.P.; Hyne, M.J.  
 Gene 53, 63-71, 1997  
 A/Title: The nucleotide sequence of the amds gene of *Aspergillus nidulans* and the molec  
 A/Reference number: A26511; MUID:87248110; PMID:9303667  
 A/Accession: A26511  
 A/Status: preliminary

A/Molecule type: mRNA  
 A/Residues: 1-548 <COR>  
 A/Cross-references: GB:M16371; NID:G168014; PIDN:AAA33295.1; PID:G168015  
 C/Superfamily: amidase

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 1; Length 548;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 296 VAALAKAG 303  
 DB 343 VAALAKAG 350

## RESULT 30

B47301  
 VirB4 homolog - *Bordetella pertussis*  
 C/Species: *Bordetella pertussis*  
 C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999  
 C/Accession: B47301  
 R/Weiss, A.A.; Johnson, F.D.; Burns, D.L.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2970-2974, 1993  
 A/Title: Molecular characterization of an operon required for pertussis toxin secretion  
 A/Reference number: A47301; MUID:93219406; PMID:8464913  
 A/Content: BP338  
 A/Accession: B47301  
 A/Status: preliminary  
 A/Molecule type: nucleic acid  
 A/Residues: 1824 <MB1>  
 A/Note: sequence extracted from NCBI backbone (NCBIN:128775, NCBIP:128777)  
 C/Superfamily: VirB4 protein

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 824;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 473 GSGKTALL 480  
 DB 459 GSGKTALL 466

## RESULT 31

T12537  
 hypothetical protein DKFZP434H244.1 - human (fragments)  
 C/Species: *Homo sapiens* (man)  
 C/Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Nov-2000  
 C/Accession: T12537  
 R/Mambrot, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, June 1999  
 A/Reference number: Z17524  
 A/Accession: T12537  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-313/314-845 <WAM>  
 A/Cross-references: EMBL:AL096750  
 A/Experimental source: adult testis; clone DKFZP434H244  
 A/Note: the cDNA sequence contains a -1 frameshift near codon 313  
 C/Genetics:  
 A/Note: DKFZP434H244.1  
 C/Superfamily: hypothetical protein YKJ215C

Query Match  
 Best Local Similarity 0.6%; Score 8; DB 2; Length 845;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 456 PEVFGNIN 463  
 DB 618 PEVFGNIN 625

## RESULT 32

T02742  
 probable ligand-gated ion channel protein [imported] - *Arabidopsis thaliana*

N/Alternate names: hypothetical protein T914.20  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 16-Feb-2001  
 C/Accession: T02742; G84692  
 R/Rounsailey, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rott  
 submitted to the EMBL Data Library, August 1998  
 A/Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.  
 A/Reference number: Z14710  
 A/Accession: T02742  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-934 <R0U>  
 A/Cross-references: EMBL:AC005315; NID:G3461834; PID:G3482941  
 A/Experimental source: cultivar Columbia  
 R/Rlin, X.; Kaul, S.; Rounsailey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 Neus, D.; Nierman, M.C.; White, O.; Bisen, O.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A/Reference number: A84420; MUID:20083487; PMID:10617197  
 A/Accession: G84692  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-934 <STO>  
 A/Cross-references: GB:AE002093; NID:G3482941; PID:AA033239.1; GSPDB:GN00139  
 C/Genetics:  
 A/Gene: T914.20; At2g29120  
 A/Map position: 2  
 A/Introns: 69/1; 514/3; 617/1; 748/3

Query Match 0.6%; Score 8; DB 2; Length 934;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 939 DKSQVPTI 946  
 DB 98 DKSQVPTI 105

RESULT 33  
 T03179  
 probable DNA-directed RNA polymerase (EC 2.7.7.6) largest chain - Chilo iridescent virus  
 N/Alternate names: DNA-dependent RNA polymerase  
 C/Species: Chilo iridescent virus  
 C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 17-Mar-2000  
 C/Accession: T03179  
 R/Bahr, U.; Tidona, C.A.; Darai, G.  
 Virus Genes 15, 235-245, 1997  
 A/Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101  
 A/Reference number: Z14834; MUID:98141693; PMID:9482589  
 A/Accession: T03179  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1026 <BAH>  
 A/Cross-references: EMBL:AF005334; NID:G2738385; PID:AA094477.1; PID:G2738450  
 C/Superfamily: Halobacterium DNA-directed RNA polymerase chain A  
 C/Keywords: DNA binding; nucleotidyltransferase; transcription; zinc finger

Query Match 0.6%; Score 8; DB 2; Length 1026;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1142 YDPSKLVK 1149  
 DB 993 YDPSKLVK 1000

RESULT 34  
 UC4889  
 phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase (EC 3.1.3.-) - human  
 N/Alternate names: hps1CN5phosphatase  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Sep-1996 #sequence\_revision 18-Oct-1996 #text\_change 05-Nov-1999

C/Accession: UC4889; PC4187  
 R/Drayer, A.L.; Pessesse, X.; De Smedt, F.; Moscholaki, R.; Parker, P.; Erneux, C.  
 Biochem. Biophys. Res. Commun. 225, 243-249, 1996  
 A/Title: Cloning and expression of a human placenta inositol 1,3,4,5-tetrakisphosphate ar  
 A/Reference number: UC4889; MUID:96332436; PMID:8769125  
 A/Content: Placenta  
 A/Accession: UC4889  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1188 <DRA>  
 A/Cross-references: EMBL:X98429; NID:G1495455; PID:CA067071.1; PID:E249440; PID:G1495455  
 A/Accession: PC4187  
 A/Molecule type: protein  
 A/Residues: 582-592; 668-675 <DR2>  
 C/Comment: This enzyme plays a function in the phosphatidylinositol 3-kinase and inositol  
 sequence motifs show that this enzyme interacts with various proteins in signal transduc  
 C/Comment: Inositol 1,3,4,5-tetrakisphosphate is also a substrate for this enzyme.  
 C/Superfamily: SH2 homology  
 C/Keywords: phosphoric monoester hydrolase  
 F/5-101/Domain: SH2 homology <SH2>  
 F/380/Binding site: substrate (Arg) #status predicted  
 F/671/Active site: Cys #status predicted

Query Match 0.6%; Score 8; DB 2; Length 1188;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1075 TLPSLESL 1082  
 DB 226 TLPSLESL 233

RESULT 35  
 UC6118  
 SH2-containing inositol phosphatase (EC 3.1.3.-) - mouse  
 N/Alternate names: Shc-associated 145K protein  
 C/Species: Mus musculus (house mouse)  
 C/Date: 23-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 12-Feb-1999  
 C/Accession: UC6118  
 R/Damen, U.B.; Liu, L.; Roosten, P.; Humphries, R.K.; Jefferson, A.B.; Majerus, P.W.; Krys  
 Proc. Natl. Acad. Sci. U.S.A. 93, 1689-1693, 1996  
 A/Title: The 145-kDa protein induced to associate with Shc by multiple cytokines is an ir  
 A/Reference number: UC6118; MUID:96202338; PMID:8643691  
 A/Accession: UC6118  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-1189 <DAM>  
 A/Cross-references: GB:U39203  
 A/Experimental source: hemopoietic cell  
 C/Comment: This enzyme is a tyrosine-phosphorylated protein. It plays an important role i  
 1b.  
 C/Superfamily: SH2 homology  
 C/Keywords: cytokine; phosphoric monoester hydrolase  
 F/8-104/Domain: SH2 homology <SH2>

Query Match 0.6%; Score 8; DB 2; Length 1189;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1075 TLPSLESL 1082  
 DB 229 TLPSLESL 236

RESULT 36  
 S74355  
 hypothetical protein sll0068 - Synechocystis sp. (strain PCC 6803)  
 C/Species: Synechocystis sp.  
 A/Variety: PCC 6803  
 C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C/Accession: S74355  
 R/Kaneh, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 A:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S74322  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1239 <NAN>  
 A:Cross-references: EMBL:D64001; GB:AB001339; NID:91001102; PIDN:BA010273.1; PID:9100113  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Superfamily: *Synechocystis* hypothetical protein e110068

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 2; Length 1239;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 GAGGSGKT 477  
 |||||  
 Db 139 GAGGSGKT 146

RESULT 37  
 T00365  
 hypothetical protein KIA0670 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Feb-1998 #sequence\_revision 01-Feb-1999 #text\_change 21-Jul-2000  
 C:Accession: T00365  
 R:Shikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.  
 DNA Res. 5, 159-176, 1998  
 A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete  
 A:Reference number: 214142; MUID:98403880; PMID:9734831  
 A:Accession: T00365  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1280 <ISH>  
 A:Cross-references: EMBL:AB014570; NID:93327153; PIDN:BA031645.1; PID:93327154  
 A:Experimental source: brain; clone HK02359  
 C:Genetics:  
 A:Note: KIA0670

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 2; Length 1280;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 EEECKR 46  
 |||||  
 Db 1195 EEECKR 1202

RESULT 38  
 F96596  
 hypothetical protein TSA14.15 (imported) - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: F96596  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 anen, N.P.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
 C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: F96596  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1360 <STO>  
 A:Cross-references: GB:AE005173; NID:94204269; PIDN:AAD10650.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: TSA14.15

A:Map position: 1

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 2; Length 1360;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 CGPLNKD 131  
 |||||  
 Db 942 CGPLNKD 949

RESULT 39  
 F86509  
 CT147 hypothetical protein (imported) - *Chlamydomonas reinhardtii* (strain J138)  
 C:Species: *Chlamydomonas reinhardtii* (strain J138)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001  
 C:Accession: F86509  
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.  
 A:Reference number: A86491; MUID:20330349; PMID:10871362  
 A:Accession: F86509  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1537 <STO>  
 A:Cross-references: GB:BA000008; NID:98978523; PIDN:BA09360.1; GSPDB:GN00142  
 A:Experimental source: strain J138  
 C:Genetics:  
 A:Gene: CP0150

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 2; Length 1537;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 LILFGAGL 109  
 |||||  
 Db 110 LILFGAGL 117

RESULT 40  
 C81558  
 conserved hypothetical protein CP0623 (imported) - *Chlamydomonas reinhardtii* (strain AR39)  
 C:Species: *Chlamydomonas reinhardtii* (strain AR39)  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 11-May-2000  
 C:Accession: C81558  
 R:Read, T.D.; Brubaker, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
 Nucleic Acids Res. 28, 1397-1406, 2000  
 A:Title: Genome sequences of *Chlamydomonas reinhardtii* and *Chlamydomonas* sp.  
 A:Reference number: A81500; MUID:20150255; PMID:10684935  
 A:Accession: C81558  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1537 <RBA>  
 A:Cross-references: GB:AE002219; GB:AE002161; NID:97189524; PIDN:AF038438.1; PID:97189533  
 A:Experimental source: strain AR39, HL cells  
 C:Genetics:  
 A:Gene: CP0623

Query Match  
 Best Local Similarity 100.0%; Score 8; DB 2; Length 1537;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 LILFGAGL 109  
 |||||  
 Db 110 LILFGAGL 117

RESULT 41  
 H72112  
 CT147 hypothetical protein - *Chlamydomonas reinhardtii* (strain CW029)  
 C:Species: *Chlamydomonas reinhardtii* (strain CW029)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-May-2000



C:Accession: H72112  
R.Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of *Clamydia pneumoniae* and *C. trachomatis*.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: H72112  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1537 <ARN>  
A:Cross-references: GB:AE001602; GB:AE001363; NID:g4376416; PIDN:AAD18303.1; PID:g437641  
A:Experimental source: strain CML028  
C:Genetics:  
A:Gene: CPN0150

Query Match 0.6%; Score 8; DB 2; Length 1537;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LILFGAGL 109  
|||||  
DB 110 LILFGAGL 117

## RESULT 42

AC0724

hypothetical protein STY1940 [imported] - *Salmonella enterica* subsp. *enterica* serovar Ty  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
A:Note: this species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AC0724  
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AC0724  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-45 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05493.1; PID:g16502997; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY1940

Query Match 0.5%; Score 7; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 327 EGDPPD 333  
|||||  
DB 27 EGDPPD 33

## RESULT 43

AF2722

hypothetical protein Atu1184 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)  
C:Species: *Agrobacterium tumefaciens*  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C:Accession: AF2722  
R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF2722  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-66 <KOR>

A:Cross-references: GB:AE008688; PIDN:AAL42196.1; PID:g17739587; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu1184  
A:Map position: circular chromosome

Query Match 0.5%; Score 7; DB 2; Length 66;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VAALAKA 302  
|||||  
DB 57 VAALAKA 63

## RESULT 44

C97504

hypothetical protein AGR\_C\_2188 [imported] - *Agrobacterium tumefaciens* (strain C58, Cerec  
C:Species: *Agrobacterium tumefaciens*  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: C97504  
R.Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,  
A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: C97504  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-72 <KOR>  
A:Cross-references: GB:AE007869; PIDN:AAK6988.1; PID:g15156228; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_2188  
A:Map position: circular chromosome

Query Match 0.5%; Score 7; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 VAALAKA 302  
|||||  
DB 63 VAALAKA 69

## RESULT 45

T50008

hypothetical protein T31P16.30 - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T50008  
R.Beyn, M.; Zimmermann, W.; Gruenewald, A.; Wambutt, R.; Kalicki, J.; Wohlmann, P.; Smi  
submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25027  
A:Accession: T50008  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-87 <BEV>  
A:Cross-references: EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.30  
A:Experimental source: cultivar Columbia; BAC clone T31P16  
C:Genetics:  
A:Gene: ATSP:T31P16.30  
A:Map position: 5

Query Match 0.5%; Score 7; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 792 LMYVSSL 798  
|||||  
DB 69 LMYVSSL 75

## RESULT 46

A13122

IS3 family transposase orfA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
 C/Accession: A13122  
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCell  
 Science 294, 2317-2323, 2001  
 A/Author: 100, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 er, E.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; MUID:21608350; PMID:11743193  
 A/Accession: A13122  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-88 <KUR>  
 A/Cross-references: GB:AE008689; PIDN:AAL45399.1; PID:917743097; GSPDB:GN00187  
 A/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Map position: linear chromosome

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 88;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SEAKRLK 65  
 |||||  
 Db 51 SEAKRLK 57

RESULT 47  
 P98164  
 Insertion element Isr1 hypothetical 10K protein A3 [imported] - Agrobacterium tumefaciens  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
 C/Accession: F98164  
 R/Goodner, B.; Hinkle, G.; Galtung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldman,  
 A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A/Reference number: A97559; MUID:21608551; PMID:11743194  
 A/Accession: F98164  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-88 <KUR>  
 A/Cross-references: GB:AE007870; PIDN:AAK8840.1; PID:915158602; GSPDB:GN00170  
 C/Genetics:  
 A/Map position: linear chromosome

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 88;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SEAKRLK 65  
 |||||  
 Db 51 SEAKRLK 57

RESULT 48  
 T35348  
 Probable membrane protein - Streptomyces coelicolor  
 C/Species: Streptomyces coelicolor  
 C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
 C/Accession: T35348  
 R/Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, May 1999  
 A/Reference number: Z21575  
 A/Accession: T35348  
 A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-89 <OLI>

A/Cross-references: EMBL:AL049863; PIDN:CAB42957.1; GSPDB:GN00070; SCOEDB:SC5H1.32  
 A/Experimental source: strain A3(2)  
 C/Genetics:  
 A/Map position: linear chromosome

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 89;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 AVGVVAL 299  
 |||||  
 Db 74 AVGVVAL 80

RESULT 49  
 B42523  
 A54L protein - vaccinia virus (strains WR and Copenhagen)  
 N/Alternate names: Salp protein  
 C/Species: Vaccinia virus  
 A/Note: host Homo sapiens (man)  
 C/Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 07-May-1999  
 C/Accession: B42523; J01825  
 R/Johnson, G.P.  
 submitted to GenBank, June 1990  
 A/Reference number: A33172  
 A/Accession: B42523  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-90 <JOH>  
 R/Smith, G.L.; Chan, Y.S.; Howard, S.T.  
 J. Gen. Virol. 72, 1349-1376, 1991  
 A/Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right im  
 A/Reference number: J01767; MUID:9125065; PMID:2045793  
 A/Accession: J01825  
 A/Molecule type: DNA  
 A/Residues: 1-90 <SMI>  
 A/Cross-references: DDBJ:D11079

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 90;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 SFFKTLN 1275  
 |||||  
 Db 43 SFFKTLN 49

RESULT 50  
 T35051  
 hypothetical protein SC4G2.16c SC4G2.16c - Streptomyces coelicolor  
 C/Species: Streptomyces coelicolor  
 C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
 C/Accession: T35051  
 R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, August 1998  
 A/Reference number: Z21566  
 A/Accession: T35051  
 A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-97 <SEB>  
 A/Cross-references: EMBL:AL031371; PIDN:CAA20553.1; GSPDB:GN00070; SCOEDB:SC4G2.16c  
 A/Experimental source: strain A3(2)  
 A/Map position: linear chromosome

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 97;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 VDEDEDL 723  
 |||||  
 Db 18 VDEDEDL 24

## RESULT 51

A39980

TYA protein - yeast (*Saccharomyces cerevisiae*) retrotransposon Ty2.917 (fragment)C/Species: *Saccharomyces cerevisiae*  
C/Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 20-Sep-1999

C/Accession: A39980

R/Liao, X.B.; Clare, J.J.; Farabaugh, P.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 8520-8524, 1987

A/Title: The upstream activation site of a Ty2 element of yeast is necessary but not sufficient for activation

A/Reference number: A39980; PMID:8808620; PMID:2825192

A/Accession: A39980

A/Molecule type: DNA

A/Residues: 1-103 &lt;LIA&gt;

A/Cross-references: GB:J18805; NID:q173114; PIDN:AAJ35187.1; PID:q173115

C/Genetics:

A/Mobile element: retrotransposon Ty2.917

C/Superfamily: TYA protein

Query Match  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 QNSPNLH 1158

DB 8 QNSPNLH 14

## RESULT 52

C69034 conserved hypothetical protein MTH1251 - *Methanobacterium thermoautotrophicum* (strain Delta H)C/Species: *Methanobacterium thermoautotrophicum*  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C/Accession: C69034

R/Smith, D.R.; Doucette-Stamm, L.A.; DeJonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadeford, R.; Viscare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A/Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functional

A/Reference number: A69000; PMID:98037514; PMID:9371463

A/Accession: C69034

A/Molecule type: DNA

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Residues: 1-103 &lt;MTH&gt;

A/Cross-references: GB:AE000891; GB:AE000666; NID:g2622345; PIDN:AA85740.1; PID:g262236

A/Experimental source: strain Delta H

C/Genetics:

A/Gene: MTH1251

Query Match  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 683 EILKATV 689

DB 19 EILKATV 25

## RESULT 53

F71681

hypothetical protein RP266 - *Rickettsia prowazekii*C/Species: *Rickettsia prowazekii*  
C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000

C/Accession: F71681

R/Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sichert-Bonten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A/Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.

A/Reference number: A71630; PMID:9903949; PMID:9823893

A/Accession: F71681

A/Molecule type: DNA

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Residues: 1-106 &lt;AND&gt;

A/Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14728.1; PID:g386082

A/Experimental source: strain Madrid E

C/Genetics:

A/Gene: RP266

Query Match  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 TVLKKI 483

DB 98 TVLKKI 104

## RESULT 54

A85639

hypothetical protein Z1446 (imported) - *Escherichia coli* (strain O157:H7, substrain EDL93)C/Species: *Escherichia coli*  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C/Accession: A85639

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoudis, K.; Apodaca, J.

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A/Reference number: A85480; PMID:21074935; PMID:11206551

A/Accession: A85639

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-113 &lt;STO&gt;

A/Cross-references: GB:AE005174; NID:g12514299; PIDN:AA655573.1; GSPDB:GN00145; UNCP:Z144

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z1446

Query Match  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1040 FIESIRP 1046

DB 18 FIESIRP 24

## RESULT 55

T49201

yippe-like protein - *Arabidopsis thaliana*

N/Alternate names: protein F27K19.70

C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000

C/Accession: T49201

R/Benes, V.; Mumbach, E.; Drzonek, H.; Anzorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z25014

A/Accession: T49201

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-121 &lt;BN&gt;

A/Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.70

A/Experimental source: cultivar Columbia; BAC clone F27K19

C/Genetics:

A/Gene: ATSP:F27K19.70

A/Map position: 3

A/Intons: 32/3; 47/2; 83/3; 102/2

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 VDLEGNI 1115

DB 7 VDLEGNI 13

## RESULT 56

H81997  
 Probable lipoprotein NMA0065 [imported] - Neisseria meningitidis (strain Z2491 serogroup C)  
 C/Species: Neisseria meningitidis  
 C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C/Accession: H81997  
 R/Patkhili, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, N.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A.; Holt, S.; Parkhill, J.; White, O.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000  
 A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A/Reference number: A81775; MUID:2022556; PMID:10761919  
 A/Accession: H81997  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-125 <PAR>  
 A/Cross-references: GB:AL162752; GB:AL157599; NID:97378778; PIDN:CAB83381.1; PID:9737883  
 A/Experimental source: serogroup A, strain Z2491  
 C/Genetics:  
 A/Gene: NMA0065  
 C/Superfamily: Neisseria meningitidis probable lipoprotein NMA0065

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 125;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 LSALLGL 29  
 DB 9 LSALLGL 15

RESULT 57  
 F81226  
 Lipoprotein, probable NMB0204 [imported] - Neisseria meningitidis (strain MCS8 serogroup C)  
 C/Species: Neisseria meningitidis  
 C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C/Accession: F81226  
 R/Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000  
 A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
 A/Reference number: A81000; MUID:20175755; PMID:10710307  
 A/Accession: F81226  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-125 <TER>  
 A/Cross-references: GB:AE002377; GB:AE002098; NID:97225416; PIDN:AAF40661.1; PID:9722542  
 A/Experimental source: serogroup B, strain MCS8  
 C/Genetics:  
 A/Gene: NMB0204  
 C/Superfamily: Neisseria meningitidis probable lipoprotein NMA0065

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 125;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 LSALLGL 29  
 DB 9 LSALLGL 15

RESULT 58  
 A82599  
 conserved hypothetical protein XP2112 [imported] - Xylella fastidiosa (strain 9ASC)  
 C/Species: Xylella fastidiosa  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C/Accession: A82599  
 R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A/Reference number: A82515; MUID:2036717; PMID:10910347  
 A/Note: for a complete list of authors see reference number A59328 below  
 A/Accession: A82599

A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-130 <STM>  
 A/Cross-references: GB:AE004026; GB:AE003849; NID:99107228; PIDN:AAF84911.1; GSPDB:GN001;  
 A/Experimental source: strain 9ASC  
 R/Simpson, A.J.G.; Reinisch, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al-Brites, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carver, H.  
 as-Neto, E.; Docena, C.; El-Doroty, H.; Faciniani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A/Authors: Pereira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitzajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Sencelici, R.V.; Sawasak  
 M.; Teshako, M.H.; Vallada, H.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A/Contents: annotation  
 C/Genetics:  
 A/Gene: XP2112

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 130;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 24 SALGLD 30  
 DB 31 SALGLD 37

RESULT 59  
 G75175  
 hypothetical protein PAB0387 - Pyrococcus abyssi (strain Orsay)  
 C/Species: Pyrococcus abyssi  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C/Accession: G75175  
 R/Anonymous, Genome  
 submitted to the EMBL Data Library, July 1999  
 A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc  
 A/Reference number: A75001  
 A/Accession: G75175  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-130 <KAW>  
 A/Cross-references: GB:AL248284; GB:AL056836; NID:95457730; PIDN:CAB49486.1; PID:el515381  
 A/Experimental source: strain Orsay  
 C/Genetics:  
 A/Gene: PAB0387

Query Match  
 Best Local Similarity 0.5%; Score 7; DB 2; Length 130;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 LAKELEE 40  
 DB 29 LAKELEE 35

RESULT 60  
 G65115  
 hypothetical 15.2 kD protein in rplM-hoa intergenic region - Escherichia coli (strain K-  
 C/Species: Escherichia coli  
 C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C/Accession: G65115  
 R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
 Science 277, 1453-1462, 1997  
 A/Title: The complete genome sequence of Escherichia coli K-12.  
 A/Reference number: A64720; MUID:97426617; PMID:9278903  
 A/Accession: G65115  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA

A:Residues: 1-134 <BLAT>  
A:Cross-references: GB:AE000402; GB:U00096; NID:g1789619; PIDN:AACT6265.1; PID:g1789628;  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: yncB  
C:Superfamily: hypothetical protein H11628

Query Match 0.5%; Score 7; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25  
DB 86 LPELSA 92

RESULT 61

B91142  
hypothetical protein ECs4106 [imported] - Escherichia coli (strain O157:H7, substrain R1

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001

C:Accession: B91142

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; PMID:11258796

A:Accession: B91142

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA837529.1; PID:g13363579; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain R1MD 0509952

C:Genetics:

A:Gene: ECs4106

C:Superfamily: hypothetical protein H11628

Query Match 0.5%; Score 7; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25  
DB 86 LPELSA 92

RESULT 62

B85987  
hypothetical protein yncB [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: B85987

R:Peria, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobleck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousie, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; PMID:11204935; PMID:11206551

A:Accession: B85987

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <STO>

A:Cross-references: GB:AE005174; NID:g12517854; PIDN:AGS8361.1; GSPDB:GN00145; UWGP:Z45

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yncB

C:Superfamily: hypothetical protein H11628

Query Match 0.5%; Score 7; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LPELSA 25  
DB 86 LPELSA 92

DB 86 LPELSA 92

RESULT 63

T42327  
hypothetical protein - phage SPPI

C:Species: phage SPPI

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-May-2000

C:Accession: T42327

R:Alonso, J.C.; Inder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.

Gene 204, 201-212, 1997

A:Title: The complete nucleotide sequence and functional organization of Bacillus subtilis

A:Reference number: Z22137; PMID:98094274; PMID:9434185

A:Accession: T42327

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-137 <ALO>

A:Cross-references: EMBL:X97918; PIDN:CAA6534.1

Query Match 0.5%; Score 7; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 INVFSYI 1121  
DB 37 INVFSYI 43

RESULT 64

C70223  
conserved hypothetical protein BBD15 - Lyme disease spirochete plasmid D/1p17

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 08-Oct-1999

C:Accession: C70223

R:Fraser, C.M.; Caojens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,

son, D.; Peterson, J.; Kervavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; PMID:98065943; PMID:9403685

A:Accession: C70223

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-140 <LDB>

A:Cross-references: GB:AE000793; NID:g2689927; PIDN:AA66348.1; PID:g2689934; TIGR:BBD15

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match 0.5%; Score 7; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 LGCGLSI 440  
DB 62 LGCGLSI 68

RESULT 65

B83611  
conserved hypothetical protein PA0269 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83611

R:Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brj

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,

.. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog

A:Reference number: A82950; PMID:10984043

A:Accession: B83611

A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-145 <STO>  
 A:Cross-references: GB:AE004465; GB:AE004091; NID:G9946107; PIDN:AA03658.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA0269

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 145;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 298 ALAKAGL 304  
 DB 24 ALAKAGL 30

RESULT 66  
 C95319  
 conserved hypothetical protein SMA0841 [imported] - *Sinorhizobium meliloti* (strain 1021)  
 C:Species: *Sinorhizobium meliloti*  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: C95319  
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
 Proc Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*  
 A:Reference number: A05262; MUID:21396509; PMID:11481432  
 A:Accession: C95319  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-149 <KUR>  
 A:Cross-references: GB:AE00469; PIDN:AAK65117.1; PID:G14523555; GSPDB:GN00165  
 R:Galibert, F.; Phan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 L.; Hyman, R.W.; Jones, T.; Davies, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kallan, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeLaure,  
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.  
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 C:Content: annotation  
 C:Genetics:  
 A:Gene: SMA0841  
 A:Genome: plasmid

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 149;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 59 SEAKRLK 65  
 DB 102 SEAKRLK 108

RESULT 67  
 B89947  
 hypothetical protein SA1469 [imported] - *Staphylococcus aureus* (strain N315)  
 C:Species: *Staphylococcus aureus*  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 14-Apr-2003  
 C:Accession: B89947  
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: B89947  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-152 <KUR>  
 A:Cross-references: GB:BA000018; PID:G13701441; PIDN:BA042735.1; GSPDB:GN00149  
 A:Experimental source: strain N315

C:Genetics:  
 A:Gene: SA1469  
 C:Superfamily: uncharacterized protein with an ACT domain

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 152;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1060 ISKLELS 1066  
 DB 94 ISKLELS 100

RESULT 68  
 S38662  
 interleukin-2 - goat  
 C:Species: *Capra aegagrus hircus* (domestic goat)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
 C:Accession: S38662  
 R:Rimstad, B.  
 submitted to the EMBL Data Library, November 1993  
 A:Description: The molecular cloning and expression of caprine interleukin 2.  
 A:Reference number: S38662  
 A:Accession: S38662  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-155 <KIM>  
 A:Cross-references: EMBL:X76063; NID:G416002; PIDN:CAA53664.1; PID:G416003  
 C:Superfamily: Interleukin-2

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 155;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1294 LENLKLS 1300  
 DB 51 LENLKLS 57

RESULT 69  
 H75028  
 probable H<sup>+</sup>-transporting two-sector ATPase (EC 3.6.3.14) proteolipid chain PAB1181 - *Pyrococcus abyssi*  
 C:Species: *Pyrococcus abyssi*  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 03-Jun-2002  
 C:Accession: H75028  
 R:anonymous, Genoscope  
 submitted to the EMBL Data Library, July 1999  
 A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome struc  
 A:Reference number: A75001  
 A:Accession: H75028  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-158 <KAW>  
 A:Cross-references: GB:A0248288; GB:AL096836; NID:G5458960; PIDN:CAB50670.1; PID:G545918  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1181  
 C:Superfamily: Na<sup>+</sup>-ATPase complex K chain  
 C:Keywords: hydrolase

Query Match  
 Best Local Similarity 100.0%; Score 7; DB 2; Length 158;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 ILFGAGL 109  
 DB 94 ILFGAGL 100

RESULT 70  
 D71214  
 hypothetical protein PH1980 - *Pyrococcus horikoshii*  
 C:Species: *Pyrococcus horikoshii*

C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
 C/Accession: D71214  
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A/Reference number: A71000; MUID:98344137; PMID:9679194  
 A/Accession: D71214  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-162 <KAW>  
 A/Cross-references: GB:AP000007; NID:93236134; PIRN:BAA31107.1; PID:93258424  
 A/Experimental source: strain OT3  
 A/Note: this accession replaces an interim accession for a sequence replaced by Genbank  
 C/Genetics:  
 A/Gene: PH1980  
 C/Superfamily: Na+-ATPase complex K chain

Query Match 0.5%; Score 7; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 IIFGAGL 109  
 |||||  
 DB 98 IIFGAGL 104

RESULT 71  
 G82322  
 dihydrofolate reductase VC0440 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
 C/Species: Vibrio cholerae  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C/Accession: G82322  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;  
 Chardon, D.; Esmolova, M.D.; Vamathevan, U.; Baes, S.; Qin, H.; Dragol, I.; Sellers, F.  
 I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A/Reference number: AB2035; MUID:20406833; PMID:10952301  
 A/Accession: G82322  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-165 <HEI>  
 A/Cross-references: GB:AE004131; GB:AE003852; NID:96654856; PIRN:AAF93613.1; GSPDB:GN001  
 C/Genetics:  
 A/Experimental source: serogroup O1; strain N16961; biotype El Tor  
 A/Gene: VC0440  
 C/Map position: 1  
 C/Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology

Query Match 0.5%; Score 7; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 AALAKAG 303  
 |||||  
 DB 82 AALAKAG 88

RESULT 72  
 S73337  
 hypothetical protein E07\_orf175 - Mycoplasma pneumoniae (strain ATCC 29342)  
 C/Species: Mycoplasma pneumoniae  
 A/Variety: ATCC 29342  
 C/Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
 C/Accession: S73337  
 R:Himmelreich, R.; Hilbert, H.; Piagene, H.; Pirkil, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A/Reference number: S73327; MUID:97105885; PMID:8948633  
 A/Accession: S73337  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA

A/Residues: 1-175 <HIM>  
 A/Cross-references: EMBL:AE000002; GB:U00089; NID:91673651; PIRN:AAB95659.1; PID:9167365;  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C/Genetics:  
 A/Gene: SGC3  
 C/Superfamily: Mycoplasma pneumoniae hypothetical protein E07\_orf175

Query Match 0.5%; Score 7; DB 2; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 523 LLEKGS 529  
 |||||  
 DB 61 LLEKGS 67

RESULT 73  
 S69636  
 hypothetical protein YDR469w - yeast (Saccharomyces cerevisiae)  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 22-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 19-Apr-2002  
 C/Accession: S69636  
 R:Dieckich, F.S.  
 submitted to the EMBL Data Library, August 1995  
 A/Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.  
 A/Reference number: S69554  
 A/Accession: S69636  
 A/Molecule type: DNA  
 A/Residues: 1-175 <DIR>  
 A/Cross-references: EMBL:U33050; NID:9927726; PID:9927731; GSPDB:GN00004; MIPS:YDR469w  
 C/Genetics:  
 A/Gene: SGD:SDC1; MIPS:YDR469w  
 A/Cross-references: SGD:S0002877  
 C/Map position: 4R  
 C/Superfamily: Saccharomyces hypothetical protein YDR469w

Query Match 0.5%; Score 7; DB 2; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 LAGMRLL 757  
 |||||  
 DB 135 LAGMRLL 141

RESULT 74  
 T49816  
 hypothetical protein B24H17.20 [imported] - Neurospora crassa  
 C/Species: Neurospora crassa  
 C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 C/Accession: T49816  
 R:Schulte, U.; Align, V.; Honeisels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 submitted to the Protein Sequence Database, May 2000  
 A/Reference number: Z25022  
 A/Accession: T49816  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-177 <SCH>  
 A/Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.20  
 A/Experimental source: BAC clone B24H17; strain OR74A  
 C/Genetics:  
 A/Gene: NCSP:B24H17.20  
 C/Map position: 6

Query Match 0.5%; Score 7; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEBOKK 45  
 |||||  
 DB 136 EEEBOKK 142

RESULT 75

B49845  
 hypothetical protein A (hema 5' region) - Rhodobacter sphaeroides  
 C:Species: Rhodobacter sphaeroides  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
 C:Accession: B49845  
 R:Neidle, E.; Kadian, S.  
 J. Bacteriol. 175, 2292-2303, 1993  
 A:Title: Expression of the Rhodobacter sphaeroides hema and hemT genes, encoding two 5-  
 A:Reference number: A49845; MUID:93224451; PMID:8468290  
 A:Contents: 2.4.1  
 A:Accession: B49845  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-189 <NEI>  
 A:Cross-references: GB:L07490; NID:G151936; PIDN:AAA7324.1; PID:G457150  
 A:Note: Sequence extracted from NCB1 backbone (NCBIN:129178, NCBIP:129179)  
 C:Superfamily: Rhodobacter sphaeroides hypothetical protein A (hema 5' region)

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 189;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	511	PDEGLAS	517
Db	72	PDEGLAS	78

Search completed: December 18, 2003, 09:15:39  
 Job time : 39 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:15:05 : Search time 285 Seconds  
(without alignments)  
919.377 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403

Sequence: 1 MATQKASDRISQPHNL.....SKYLTIQKWLPEPPIQK 1403

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 696363 seqs, 186758610 residues

Word size : 0

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCNT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCNTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403	100.0	1403	8	US-08-913-322-22
2	1403	100.0	1403	8	US-08-913-322-24
3	1403	100.0	1403	15	US-10-285-408-1
4	496	35.4	782	9	US-09-841-739-9
5	496	35.4	782	12	US-10-449-315-9
6	385	27.4	385	12	US-10-029-386-33707
7	203	14.5	203	12	US-10-029-386-33933
8	75	5.3	118	9	US-09-925-299-1033
9	75	5.3	118	11	US-09-925-299-1033
10	50	3.6	50	15	US-10-138-618-26
11	47	3.3	47	15	US-10-138-618-13
12	22	1.6	37	9	US-09-864-761-47337
13	12	0.9	898	9	US-09-841-739-11
14	12	0.9	898	12	US-10-449-315-11
15	8	0.6	15	9	US-09-812-471-20

16	8	0.6	15	10	US-09-812-633-20	Sequence 20, Appl
17	8	0.6	15	10	US-09-988-117-20	Sequence 20, Appl
18	8	0.6	64	12	US-09-933-767-580	Sequence 580, Appl
19	8	0.6	64	15	US-10-023-282-580	Sequence 580, Appl
20	8	0.6	68	10	US-09-201-936-16	Sequence 16, Appl
21	8	0.6	95	9	US-09-925-297-743	Sequence 743, Appl
22	8	0.6	201	15	US-10-156-761-8837	Sequence 8837, Ap
23	8	0.6	259	9	US-09-925-299-821	Sequence 821, App
24	8	0.6	259	11	US-09-925-299-821	Sequence 821, App
25	8	0.6	481	15	US-10-156-761-12012	Sequence 12012, A
26	8	0.6	496	10	US-09-974-592-10	Sequence 10, Appl
27	8	0.6	496	10	US-09-201-936-10	Sequence 10, Appl
28	8	0.6	567	12	US-09-933-767-573	Sequence 573, App
29	8	0.6	567	15	US-10-023-282-573	Sequence 573, App
30	8	0.6	667	9	US-09-864-761-455	Sequence 55, Appl
31	8	0.6	667	11	US-09-728-644-55	Sequence 55, Appl
32	8	0.6	976	10	US-09-969-528-2	Sequence 2, Appl1
33	8	0.5	7	12	US-10-291-607-15	Sequence 15, Appl
34	7	0.5	10	9	US-09-812-471-15	Sequence 15, Appl
35	7	0.5	10	10	US-09-812-633-15	Sequence 15, Appl
36	7	0.5	10	10	US-09-988-117-15	Sequence 15, Appl
37	7	0.5	14	9	US-09-812-471-14	Sequence 14, Appl
38	7	0.5	14	10	US-09-812-633-14	Sequence 14, Appl
39	7	0.5	14	10	US-09-988-117-14	Sequence 14, Appl
40	7	0.5	16	9	US-09-812-471-13	Sequence 13, Appl
41	7	0.5	16	10	US-09-812-633-13	Sequence 13, Appl
42	7	0.5	16	10	US-09-988-117-13	Sequence 13, Appl
43	7	0.5	20	9	US-09-812-471-10	Sequence 10, Appl
44	7	0.5	20	10	US-09-812-633-10	Sequence 10, Appl
45	7	0.5	20	10	US-09-988-117-10	Sequence 10, Appl
46	7	0.5	42	9	US-09-726-643-145	Sequence 145, App
47	7	0.5	42	14	US-10-042-141-145	Sequence 145, App
48	7	0.5	48	12	US-10-232-286-9	Sequence 9, Appl1
49	7	0.5	50	10	US-09-071-838-94	Sequence 94, Appl
50	7	0.5	50	15	US-10-138-618-21	Sequence 21, Appl
51	7	0.5	50	15	US-10-138-618-31	Sequence 31, Appl
52	7	0.5	50	15	US-10-138-618-31	Sequence 31, Appl
53	7	0.5	50	15	US-10-213-512-94	Sequence 94, Appl
54	7	0.5	52	9	US-09-864-761-43582	Sequence 43582, A
55	7	0.5	56	9	US-09-864-761-47236	Sequence 47236, A
56	7	0.5	56	15	US-10-156-761-8279	Sequence 8279, Ap
57	7	0.5	56	15	US-10-156-761-8496	Sequence 8496, Ap
58	7	0.5	64	9	US-09-864-761-16549	Sequence 4549, A
59	7	0.5	66	9	US-09-864-761-43318	Sequence 43318, A
60	7	0.5	67	10	US-09-201-936-23	Sequence 23, Appl
61	7	0.5	68	10	US-09-201-936-27	Sequence 27, Appl
62	7	0.5	68	15	US-10-041-859-15	Sequence 15, Appl
63	7	0.5	68	15	US-10-041-859-15	Sequence 15, Appl
64	7	0.5	69	9	US-09-864-761-44802	Sequence 44802, A
65	7	0.5	91	15	US-10-106-698-4757	Sequence 4757, Ap
66	7	0.5	91	12	US-10-029-386-30446	Sequence 30446, A
67	7	0.5	99	9	US-09-864-761-38254	Sequence 38254, A
68	7	0.5	101	9	US-09-864-761-34814	Sequence 34814, A
69	7	0.5	102	9	US-09-864-761-39550	Sequence 39550, A
70	7	0.5	107	15	US-10-156-761-8010	Sequence 8010, Ap
71	7	0.5	109	9	US-09-867-550-1404	Sequence 1404, Ap
72	7	0.5	130	12	US-10-029-386-32489	Sequence 32489, A
73	7	0.5	134	12	US-10-287-274-415	Sequence 415, App
74	7	0.5	139	9	US-09-815-242-5364	Sequence 5364, App
75	7	0.5	144	15	US-10-156-761-14188	Sequence 14188, A
76	7	0.5	152	9	US-09-815-242-12642	Sequence 12642, A
77	7	0.5	152	9	US-09-815-242-12879	Sequence 12879, A
78	7	0.5	172	15	US-10-041-859-9	Sequence 9, Appl1
79	7	0.5	172	15	US-10-041-859-10	Sequence 10, Appl
80	7	0.5	197	15	US-10-156-761-8904	Sequence 8904, App
81	7	0.5	197	15	US-10-156-761-367	Sequence 367, App
82	7	0.5	198	9	US-09-925-301-1184	Sequence 1184, Ap
83	7	0.5	198	15	US-10-106-698-5870	Sequence 5870, Ap
84	7	0.5	202	11	US-09-791-279-190	Sequence 190, App
85	7	0.5	207	9	US-09-925-301-1160	Sequence 1160, App
86	7	0.5	209	9	US-09-925-301-931	Sequence 931, App
87	7	0.5	222	12	US-10-091-007-58	Sequence 58, Appl
88	7	0.5	234	9	US-09-764-898-202	Sequence 202, Appl

[illegible]

RESULT 1  
US-08-913-322-22

Query Match	100.0%;	Score 1403;	DB 8;	Length 1403;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1403; Conservative	0.000000			

361 RGELCELLETBESNLESIANGVIVEMAGEQWFOEAKNOLNOLRAATSAFRMS 420  
421 LUDISDLTTHLACDLSISAKHISKPOVEPIVLEVEGGINASWYCWEGSAGSKTVLL 480  
422 LUDISSDLATHLACDLSISAKHISKPOVEPIVLEVEGGINASWYCWEGSAGSKTVLL 480  
481 KXIAFLMASGCCPLNFFOLVFIYLSISRPBGLASITICOLLKEGSAVTEMOMRIIO 540  
481 KXIAFLMASGCCPLNFFOLVFIYLSISRPBGLASITICOLLKEGSAVTEMOMRIIO 540  
541 QKNOQVLELUDYEICSDIOVIGKIQKMLSRPTCLIAVTRRADIRRYLETLEK 600  
541 QKNOQVLELUDYEICSDIOVIGKIQKMLSRPTCLIAVTRRADIRRYLETLEK 600  
601 AFFPYNVCLRLFSHNATRLRKEMVYFGKNOISLOKITPFLVAICAHMFOYFPDPS 660  
601 AFFPYNVCLRLFSHNATRLRKEMVYFGKNOISLOKITPFLVAICAHMFOYFPDPS 660  
661 PDDVNAFYSYMERLSIRNKATATLILKATVSSCEBLAKGFSCCFEPNDDLAEGVDED 720  
661 PDDVNAFYSYMERLSIRNKATATLILKATVSSCEBLAKGFSCCFEPNDDLAEGVDED 720  
721 EDULMCLMSKPAQGLRPYRFUSPAQETLAQMLILBILDSROREHDLGLYHLKINS 780  
721 EDULMCLMSKPAQGLRPYRFUSPAQETLAQMLILBILDSROREHDLGLYHLKINS 780  
781 PMMTVASANNFLANVSSLBSTKAGPRTIVSHLHLVDNKESJENISENDVTLKQPEISIQ 840  
781 PMMTVASANNFLANVSSLBSTKAGPRTIVSHLHLVDNKESJENISENDVTLKQPEISIQ 840  
841 MOLLRGMLQICPOAFESWSEHLVLTALCTAIVOSNTVAASCPFLQPLQGRVTLTGALNL 900  
841 MOLLRGMLQICPOAFESWSEHLVLTALCTAIVOSNTVAASCPFLQPLQGRVTLTGALNL 900  
901 QYFDPHESLSLRSIHPIRINKTSPRANHVSULETCFDKSQVPTIDDOYASAFERNHEW 960  
901 QYFDPHESLSLRSIHPIRINKTSPRANHVSULETCFDKSQVPTIDDOYASAFERNHEW 960  
961 ERNLAKEEDNVASVYMDMRAPSPULSTGYWMLSPKOYKIPCLEVDVNDIDVQGMDETL 1020  
961 ERNLAKEEDNVASVYMDMRAPSPULSTGYWMLSPKOYKIPCLEVDVNDIDVQGMDETL 1020  
1021 MTFVSAOSIEHLNHSKGFIESIRPALTELKSAVYKCSISKLELSAABOELITLPSLR 1080  
1021 MTFVSAOSIEHLNHSKGFIESIRPALTELKSAVYKCSISKLELSAABOELITLPSLR 1080  
1081 SLEVSQGTIOQODOIFPNLDKFLCKELSAVDLEGNINVSVPREEPNFHNEXKLLIOISA 1140  
1081 SLEVSQGTIOQODOIFPNLDKFLCKELSAVDLEGNINVSVPREEPNFHNEXKLLIOISA 1140  
1141 EYDPSKVLKVLIONSPPNLAHPHLKCNFESDFGSLMTMLVSCCKLTELIFSDSPFOAEPVA 1200  
1141 EYDPSKVLKVLIONSPPNLAHPHLKCNFESDFGSLMTMLVSCCKLTELIFSDSPFOAEPVA 1200  
1201 SLNPNFSLKTLNLEGOQFDEBESKEXAVIIGLSJNLSEILITPGSIGRYAVKLLIOCOQ 1260  
1201 SLNPNFSLKTLNLEGOQFDEBESKEXAVIIGLSJNLSEILITPGSIGRYAVKLLIOCOQ 1260  
1261 QMLCHLWLSAFFTLNDDSVETAKAVASGGFOKLEMLKINSIHKKTTEBGYNRFOALDNM 1320  
1261 QMLCHLWLSAFFTLNDDSVETAKAVASGGFOKLEMLKINSIHKKTTEBGYNRFOALDNM 1320  
1321 PNIQSLDISRHRTETCIRKQATTVVASLOCRLRPLIRLMLSMWLDADDIALNWKER 1380  
1321 PNIQSLDISRHRTETCIRKQATTVVASLOCRLRPLIRLMLSMWLDADDIALNWKER 1380  
1381 HFOSKYTLITLQKWLIPSPITOK 1403  
1381 HFOSKYTLITLQKWLIPSPITOK 1403

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US-08-913-322-24
; Sequence 24, Application US/08913322
; Publication No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; TITLE OF INVENTION: (NAIP)
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: GB 9601108.5
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1403
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-913-322-24

Query Match      100.0%; Score 1403; DB 8; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELSEEBEQERAKOMQGYNSQMRSE 60
DB      1 MATOQKASDERISQFDHNLPELSALLGLDAVOLAKELSEEBEQERAKOMQGYNSQMRSE 60
QY      61 AKRLKTYVYTPYSSWIPQEMAAAGFTYGYSGIQCFCCSLIFGAGLTRLPEDHKRF 120
DB      61 AKRLKTYVYTPYSSWIPQEMAAAGFTYGYSGIQCFCCSLIFGAGLTRLPEDHKRF 120
QY      121 HPDGGFLANDVGNIAIYDRIKVKLKSRLGCKMKRYOEBEARLASFRNMPYVYGISPCV 180
DB      121 HPDGGFLANDVGNIAIYDRIKVKLKSRLGCKMKRYOEBEARLASFRNMPYVYGISPCV 180
QY      121 HPDGGFLANDVGNIAIYDRIKVKLKSRLGCKMKRYOEBEARLASFRNMPYVYGISPCV 180
DB      121 HPDGGFLANDVGNIAIYDRIKVKLKSRLGCKMKRYOEBEARLASFRNMPYVYGISPCV 180
QY      181 LSEAGFVFTGKODTVQFCGCGCLGNWEGDDPWKEHAKWPKCEPLRSKSSSEITQYI 240
DB      181 LSEAGFVFTGKODTVQFCGCGCLGNWEGDDPWKEHAKWPKCEPLRSKSSSEITQYI 240
QY      241 QSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVAALA 300
DB      241 QSYKGFVDITGEHFVNSWVORELPMASAYCNDISIFAYBELRLDSFKDMPRESAVGVAALA 300
QY      301 KAGLFYTGIDIVOCFCGCGCLGKEMOGDDPLDHTCCFPNCPFLQNMKSSAETPDLQS 360
DB      301 KAGLFYTGIDIVOCFCGCGCLGKEMOGDDPLDHTCCFPNCPFLQNMKSSAETPDLQS 360
QY      361 RGEICELLETTSESNLSDSIKAVGPIVPEMAQGEAQMFOEAKNLEOQRAATTSAPRHS 420
DB      361 RGEICELLETTSESNLSDSIKAVGPIVPEMAQGEAQMFOEAKNLEOQRAATTSAPRHS 420
QY      421 LLDISSDLATDHLIGCDLSIASKHSKRPVQEPVLPEVFGNLNSVMCEBAGSGKTVLL 480
DB      421 LLDISSDLATDHLIGCDLSIASKHSKRPVQEPVLPEVFGNLNSVMCEBAGSGKTVLL 480
QY      481 KKTAFWASGCCPLNRFQVLYSLSTRPDEGLASITCOQLLEKGSVTEMCMRNIIQ 540
DB      481 KKTAFWASGCCPLNRFQVLYSLSTRPDEGLASITCOQLLEKGSVTEMCMRNIIQ 540
QY      541 QLNQVFLFLDDYKEICSIPOVIGKLIQKHLSTRCLLIAVTRARADIRRYLETIIEIK 600
DB      541 QLNQVFLFLDDYKEICSIPOVIGKLIQKHLSTRCLLIAVTRARADIRRYLETIIEIK 600
QY      601 APPRYNTVCILRKLFSSHMTRLKRFMYFGKNSLOKI QKTPLFVAALCAHMFQYPPDS 660
DB      601 APPRYNTVCILRKLFSSHMTRLKRFMYFGKNSLOKI QKTPLFVAALCAHMFQYPPDS 660

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QY      661 FDDVAVEKSYMERLSLNKATATILKATVSSCGELALKGFPSCCFBFRNDLDLAEGYDDE 720
DB      661 FDDVAVEKSYMERLSLNKATATILKATVSSCGELALKGFPSCCFBFRNDLDLAEGYDDE 720
QY      721 EDLTMCLMSKFTQORLEPPYRPLSPAFQEFLAGKRLIELLSDSROEODLGLYHLKOINS 780
DB      721 EDLTMCLMSKFTQORLEPPYRPLSPAFQEFLAGKRLIELLSDSROEODLGLYHLKOINS 780
QY      781 PMMTVSAYNNPFLNVSLSPTKAGPKTVSHLHLVNDKSELNSENDDVYLKQOPELSIQ 840
DB      781 PMMTVSAYNNPFLNVSLSPTKAGPKTVSHLHLVNDKSELNSENDDVYLKQOPELSIQ 840
QY      841 MOLLRGHMOICPOAYFSEVSEHLLVTLAKTAYOSNTYAASPPVLOPLQGRITLIGALNTL 900
DB      841 MOLLRGHMOICPOAYFSEVSEHLLVTLAKTAYOSNTYAASPPVLOPLQGRITLIGALNTL 900
QY      901 QYFEDHESLSLRSIHPIRGNTSFRHAFSVLETFCDSQVPTIDODYASAEPMNEM 960
DB      901 QYFEDHESLSLRSIHPIRGNTSFRHAFSVLETFCDSQVPTIDODYASAEPMNEM 960
QY      961 ERNLAEKEDNVKSYMDOQRASPLSLSTGYKLSPKQYKICPLEVDVNDIDVQGMLEIL 1020
DB      961 ERNLAEKEDNVKSYMDOQRASPLSLSTGYKLSPKQYKICPLEVDVNDIDVQGMLEIL 1020
QY      1021 MTVPASASQRIEHLNHSRGFTESIRPALDELKASVTCSISKLELSAEOELTLPSLE 1080
DB      1021 MTVPASASQRIEHLNHSRGFTESIRPALDELKASVTCSISKLELSAEOELTLPSLE 1080
QY      1081 SLEVSGTIOGODOIFPNLDRFLCLKELSVDLEGNINVSFVYPEEPNPHHMKLLIOISA 1140
DB      1081 SLEVSGTIOGODOIFPNLDRFLCLKELSVDLEGNINVSFVYPEEPNPHHMKLLIOISA 1140
QY      1141 EYDPSKLVKLIQNSPNLHVHLKCNFSDPSGLMTHLVSCCKLTELFRSDFPAVFPVA 1200
DB      1141 EYDPSKLVKLIQNSPNLHVHLKCNFSDPSGLMTHLVSCCKLTELFRSDFPAVFPVA 1200
QY      1201 SLNPFISLKLINLEGOQFPDEETSEKFAVYIIGLSINLEELILPTGDIYRVAKLIIOCCQ 1260
DB      1201 SLNPFISLKLINLEGOQFPDEETSEKFAVYIIGLSINLEELILPTGDIYRVAKLIIOCCQ 1260
QY      1261 QHCLARVLSFPTKLNDSVVEIAKVAISGFOKLEBNLKSINHKTIEGYRNPFOALDNM 1320
DB      1261 QHCLARVLSFPTKLNDSVVEIAKVAISGFOKLEBNLKSINHKTIEGYRNPFOALDNM 1320
QY      1321 PNLQELDISRHFTBCIAQATTVKSLSQCTVLRPLRLNMLSWLMDADIDALANVKKER 1380
DB      1321 PNLQELDISRHFTBCIAQATTVKSLSQCTVLRPLRLNMLSWLMDADIDALANVKKER 1380
QY      1381 HPOSKYTLTIQKMLPSPPIIOK 1403
DB      1381 HPOSKYTLTIQKMLPSPPIIOK 1403

RESULT 3
US-10-285-408-1
; Sequence 1, Application US/10285408
; Publication No. US20030108967A1
; GENERAL INFORMATION:
; APPLICANT: Ikeda, Johne
; APPLICANT: SAKAI, Harumi
; TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein 1
; TITLE OF INVENTION: and Method For Assaying the NAIP
; FILE REFERENCE: 2002-1440/MWC/00653
; CURRENT APPLICATION NUMBER: US/10/285,408
; EARLIER FILING DATE: 2002-11-01
; EARLIER APPLICATION NUMBER: 09/830,338
; EARLIER FILING DATE: 2001-04-26
; EARLIER APPLICATION NUMBER: PCT/JP99/05841
; EARLIER FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 1403

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TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-285-408-1

Query Match  
Best Local Similarity 100.0%; Score 1403; DB 15; Length 1403;  
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MATOQKASDERISQFHNILPELSALGLDVAOLAKELEBEEBOKERAMOKGVNSQWSE 60
1 MATOQKASDERISQFHNILPELSALGLDVAOLAKELEBEEBOKERAMOKGVNSQWSE 60
61 AKDLKFTYEPYSSSIPOEMAAAGFTYGVSGIGCCSLLIFGGLTRLPJEDHKRF 120
61 AKDLKFTYEPYSSSIPOEMAAAGFTYGVSGIGCCSLLIFGGLTRLPJEDHKRF 120
121 HPDCCFLNKDVGNIAKTDIVKULKSLRGKRRYQEEBARIASPRNPFYVQGISPCV 180
121 HPDCCFLNKDVGNIAKTDIVKULKSLRGKRRYQEEBARIASPRNPFYVQGISPCV 180
181 LSEAGFVFTGKODTYQCSGCGCLGNWEGDDPMKSHAKMPKCEPLASKSSSEITQYI 240
181 LSEAGFVFTGKODTYQCSGCGCLGNWEGDDPMKSHAKMPKCEPLASKSSSEITQYI 240
241 QSYKGFVDITGEHFVNSWVORELPMAISAYCNSDIFAYEELRDSFKDWPRESAVGVALA 300
241 QSYKGFVDITGEHFVNSWVORELPMAISAYCNSDIFAYEELRDSFKDWPRESAVGVALA 300
301 KAGLFYTGIDIVQSCCGGCLGKQWEGDDPLDHTRCFPCNCPFQNMKSSAEVTPDLOS 360
301 KAGLFYTGIDIVQSCCGGCLGKQWEGDDPLDHTRCFPCNCPFQNMKSSAEVTPDLOS 360
361 RGEICELLETTSSESNEDSIAVGPVPEMAQGEQWPEANLNEQLRAAYTSASFRHMS 420
361 RGEICELLETTSSESNEDSIAVGPVPEMAQGEQWPEANLNEQLRAAYTSASFRHMS 420
421 LLDISSDLATDHLGCDLSIASKHSKRVQEPVLPVFNGLNSVWCVGEAGSGKTYLL 480
421 LLDISSDLATDHLGCDLSIASKHSKRVQEPVLPVFNGLNSVWCVGEAGSGKTYLL 480
481 KKIATFLMASGCCPLNRQVLVYISLSSTRPDEGLASIIICDULEKESGVTEMCKRNIIQ 540
481 KKIATFLMASGCCPLNRQVLVYISLSSTRPDEGLASIIICDULEKESGVTEMCKRNIIQ 540
541 QLKQOVFLDDYKEICISIPQVIGKLIQKXHSRTCLLAVTNRARDIRRYETILEIK 600
541 QLKQOVFLDDYKEICISIPQVIGKLIQKXHSRTCLLAVTNRARDIRRYETILEIK 600
601 AFPPYNTVCILRLKFSHNMTRLRKFMVYFGKQNSIQIKTLPVVAICAHMFQYPPDPS 660
601 AFPPYNTVCILRLKFSHNMTRLRKFMVYFGKQNSIQIKTLPVVAICAHMFQYPPDPS 660
661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELATKGFSCCFEPNDDDLAEGVDED 720
661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELATKGFSCCFEPNDDDLAEGVDED 720
721 EDLTWCLMSKFTAORLRPFYRFLSPAFOEFLAGRLIELLDSROEHODLGLYHKQNS 780
721 EDLTWCLMSKFTAORLRPFYRFLSPAFOEFLAGRLIELLDSROEHODLGLYHKQNS 780
781 PMMTVSAYNNPLNYVSSLPSTKAGPKIVSHLHLVYNNKSLKXISNDYLYKHQBEISIQ 840
781 PMMTVSAYNNPLNYVSSLPSTKAGPKIVSHLHLVYNNKSLKXISNDYLYKHQBEISIQ 840
841 MOLLRLGMLQICPOAYFMSVSEHLVYALKTAYOSNTVAACSPFVLOFLOGRTLLGLANL 900
841 MOLLRLGMLQICPOAYFMSVSEHLVYALKTAYOSNTVAACSPFVLOFLOGRTLLGLANL 900
901 QYFDDHESISLRSIHPRIKGNKSPRAHFSVLETCFDSQVPIPIODDYASAEPPNENW 960
901 QYFDDHESISLRSIHPRIKGNKSPRAHFSVLETCFDSQVPIPIODDYASAEPPNENW 960
961 ERNLAEKEDNVKSYMQRASPDLSGTWKLSPQYKIPCLGVNDVNDIVVQDMLEIL 1020

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961 ERNLAEKEDNVKSYMQRASPDLSGTWKLSPQYKIPCLGVNDVNDIVVQDMLEIL 1020
1021 MTVSASORIEILNLSRGPISIRPALELSKASATYKISIKLELSAADELLITPLSLE 1080
1021 MTVSASORIEILNLSRGPISIRPALELSKASATYKISIKLELSAADELLITPLSLE 1080
1081 SLEVSQTIOSQOQIFPNLDKFLCKELSVLDEGNINPVSYIPPEFPFHMEKLLIQISA 1140
1081 SLEVSQTIOSQOQIFPNLDKFLCKELSVLDEGNINPVSYIPPEFPFHMEKLLIQISA 1140
1141 EYDPSLTVLQNSPNLAVFHLKCNPFSDGSLMTMLVSCSKLTETKFSDFQAVPFA 1200
1141 EYDPSLTVLQNSPNLAVFHLKCNPFSDGSLMTMLVSCSKLTETKFSDFQAVPFA 1200
1201 SUPNFIISLKIINLEGOQFPDEBTESEKFAVILGSLNLEELLPDGDGIYRAVKLLIQCCQ 1260
1201 SUPNFIISLKIINLEGOQFPDEBTESEKFAVILGSLNLEELLPDGDGIYRAVKLLIQCCQ 1260
1261 QHCLRVLSFPKTLNDSVVEIAKVAISGFOKLENTKLSINHKTTERGYNFOALDNM 1320
1261 QHCLRVLSFPKTLNDSVVEIAKVAISGFOKLENTKLSINHKTTERGYNFOALDNM 1320
1321 PNLDELISHHFEKCAQATYKSLSQCVLRPLRLNMLSWLDDADLIALNWKER 1380
1321 PNLDELISHHFEKCAQATYKSLSQCVLRPLRLNMLSWLDDADLIALNWKER 1380
1381 HPOSKYTLTIQKWLFPFSPIIOK 1403
1381 HPOSKYTLTIQKWLFPFSPIIOK 1403

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RESULT 4  
US-09-841-739-9  
Sequence 9, Application US/09841739  
Patent No. US20020034784A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-329001  
CURRENT APPLICATION NUMBER: US/09/841, 739  
CURRENT FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: US 03/697, 089  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161, 822  
PRIOR FILING DATE: 1999-10-27  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PASCSEQ for windows Version 4.0  
SEQ ID NO 9  
LENGTH: 782  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-841-739-9

Query Match  
Best Local Similarity 35.4%; Score 496; DB 9; Length 782;  
Matches 656; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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451 EPLVLPPEYFGLNLSVWCVGEAGSGKTYLLKIIATFLMASGCCPLNRQVLVYISLSSTR 510
1 EPLVLPPEYFGLNLSVWCVGEAGSGKTYLLKIIATFLMASGCCPLNRQVLVYISLSSTR 510
511 PDEGLASIIICDULEKESGVTEMCKRNIIQKQNOVFLDDYKEICISIPQVIGKLIQKN 570
61 PDEGLASIIICDULEKESGVTEMCKRNIIQKQNOVFLDDYKEICISIPQVIGKLIQKN 570
571 HLRSTCLLAVTNRARDIRRYLETILEIKAFPPYNTVCILRLKFSHNMTRLRKFMVYFG 630
121 HLRSTCLLAVTNRARDIRRYLETILEIKAFPPYNTVCILRLKFSHNMTRLRKFMVYFG 630
631 KNSLSQIKTQKTPLFVAALCAHMFQYPPDPSFDDVAVFKSYMERLSLRNKATAEILKATVS 690
181 KNSLSQIKTQKTPLFVAALCAHMFQYPPDPSFDDVAVFKSYMERLSLRNKATAEILKATVS 690

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Qy 691 SCGELALKEGFFSCCFEENDDDLAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 750
Db 241 SCGELALKEGFFSCCFEENDDDLAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 306
Qy 751 LAGRLIELLDSROEHQDGLYHLKQINSPPMTVSAVNNFLVYSSLPTKAGPKIVSH 810
Db 301 LAGRLIELLDSROEHQDGLYHLKQINSPPMTVSAVNNFLVYSSLPTKAGPKIVSH 360
Qy 811 LHLVNDKESLEINSENDVTLKHQPEISLQMOILRGIMQICPOAFYFMSVSEHLVTLAKT 870
Db 361 LHLVNDKESLEINSENDVTLKHQPEISLQMOILRGIMQICPOAFYFMSVSEHLVTLAKT 420
Qy 871 AYOSNTVAACSPFVLQFLQGRITLTLGALNQLYFFDHESLSLRSIHFP1RGNTSPRAH 930
Db 421 AYOSNTVAACSPFVLQFLQGRITLTLGALNQLYFFDHESLSLRSIHFP1RGNTSPRAH 480
Qy 931 FSVLETGCFDQSQVPTTIDQDYASAFEPNNEWRNLAEKEDNVKSYMQRASPDLSGTGYW 990
Db 481 FSVLETGCFDQSQVPTTIDQDYASAFEPNNEWRNLAEKEDNVKSYMQRASPDLSGTGYW 540
Qy 991 KLSPKQYKICLEVDVNDIVVGDMLIEMTVFSASORIELHNSRGFTESIRPALTEL 1050
Db 541 KLSPKQYKICLEVDVNDIVVGDMLIEMTVFSASORIELHNSRGFTESIRPALTEL 600
Qy 1051 SKASVTKCSISKLELSAEOELLTLPSLESLEVSQGTIGSODQIFPMLDKFLCKELSYD 1110
Db 601 SKASVTKCSISKLELSAEOELLTLPSLESLEVSQGTIGSODQIFPMLDKFLCKELSYD 660
Qy 1111 LEGNINVSIVIPPEFPNFMHEKLLIQISAEDPSKLV 1148
Db 661 LEGNINVSIVIPPEFPNFMHEKLLIQISAEDPSKLV 698

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RESULT 5  
US-10-449-315-9

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; Sequence 9, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Bettin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449, 315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US /09/841, 739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-9

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Query Match 35.4%; Score 496; DB 12; Length 782;  
Best local similarity 99.7%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 451 EPLVLPVFGNLSVNCVGEAGSGKTVLTKIAFLWASGCCPLNPFQVLYFSLSTR 510
Db 1 EPLVLPVFGNLSVNCVGEAGSGKTVLTKIAFLWASGCCPLNPFQVLYFSLSTR 60
Qy 511 PDGELASIIICDQLEKEGSVTEMCRNIIQOLKQVFLDDYGEISIQVIGKLIQKN 570
Db 61 PDGELASIIICDQLEKEGSVTEMCRNIIQOLKQVFLDDYGEISIQVIGKLIQKN 120
Qy 571 HLSRTCLIAVTRNARDIRRYETLIEIKAFPPYNTVCILRKLFSHNMTRLRKFMVYFG 630
Db 121 HLSRTCLIAVTRNARDIRRYETLIEIKAFPPYNTVCILRKLFSHNMTRLRKFMVYFG 180

```

```

Qy 631 KNSLOKIQKTPLEVAICAMFQYPPSPDDVAVKSVMERLSLNKATATILKATVS 690
Db 161 KNSLOKIQKTPLEVAICAMFQYPPSPDDVAVKSVMERLSLNKATATILKATVS 240
Qy 691 SCGELALKEGFFSCCFEENDDDLAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 750
Db 241 SCGELALKEGFFSCCFEENDDDLAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 300
Qy 751 LAGRLIELLDSROEHQDGLYHLKQINSPPMTVSAVNNFLVYSSLPTKAGPKIVSH 810
Db 301 LAGRLIELLDSROEHQDGLYHLKQINSPPMTVSAVNNFLVYSSLPTKAGPKIVSH 360
Qy 811 LHLVNDKESLEINSENDVTLKHQPEISLQMOILRGIMQICPOAFYFMSVSEHLVTLAKT 870
Db 361 LHLVNDKESLEINSENDVTLKHQPEISLQMOILRGIMQICPOAFYFMSVSEHLVTLAKT 420
Qy 871 AYOSNTVAACSPFVLQFLQGRITLTLGALNQLYFFDHESLSLRSIHFP1RGNTSPRAH 930
Db 421 AYOSNTVAACSPFVLQFLQGRITLTLGALNQLYFFDHESLSLRSIHFP1RGNTSPRAH 480
Qy 931 FSVLETGCFDQSQVPTTIDQDYASAFEPNNEWRNLAEKEDNVKSYMQRASPDLSGTGYW 990
Db 481 FSVLETGCFDQSQVPTTIDQDYASAFEPNNEWRNLAEKEDNVKSYMQRASPDLSGTGYW 540
Qy 991 KLSPKQYKICLEVDVNDIVVGDMLIEMTVFSASORIELHNSRGFTESIRPALTEL 1050
Db 541 KLSPKQYKICLEVDVNDIVVGDMLIEMTVFSASORIELHNSRGFTESIRPALTEL 600
Qy 1051 SKASVTKCSISKLELSAEOELLTLPSLESLEVSQGTIGSODQIFPMLDKFLCKELSYD 1110
Db 601 SKASVTKCSISKLELSAEOELLTLPSLESLEVSQGTIGSODQIFPMLDKFLCKELSYD 660
Qy 1111 LEGNINVSIVIPPEFPNFMHEKLLIQISAEDPSKLV 1148
Db 661 LEGNINVSIVIPPEFPNFMHEKLLIQISAEDPSKLV 698

```

RESULT 6  
US-10-029-386-33707

```

; Sequence 33707, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Labeling Engine vers. 1.1
; SEQ ID NO 33707
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO UB0017.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
; OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALU0 0.00e+00
US-10-029-386-33707

```

Query Match 27.4%; Score 385; DB 12; Length 385;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 707 FNDDDLAAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 766
Db 1 FNDDDLAAAGVDEDEDLTMCMSKFTAQRLRPYRFLSPAFQEF 60
Qy 767 HODLGLYHLKQINSPPMTVSAVNNFLVYSSLPTKAGPKIVSHLHLVNDKESLEINIS 826

```

```

Db      61  HODDLVYHLKQINSFMTVSAVNNFLNVSSLPSTKAGPKIVSHLHLVNDKESLENISE 120
Qy      827  NDDYKHPHPEISLQWQLRLGLMOICPOAFSVMSEHLVATLCTAVQSTVAAACSPFVLQ 886
Db      121  NDDYKHPHPEISLQWQLRLGLMOICPOAFSVMSEHLVATLCTAVQSTVAAACSPFVLQ 180
Qy      887  FLOGRRTLLGLANLQYEPDPHPEISLRLSHPIRGNKTSPPRAHFSVLETCFDSQVPTI 946
Db      181  FLOGRRTLLGLANLQYEPDPHPEISLRLSHPIRGNKTSPPRAHFSVLETCFDSQVPTI 240
Qy      947  DQDVASAFEPNNENWERNLAEKEDNVKSYNDMQRASPDLSITGYMLSPQYKIPCLFEDV 1006
Db      241  DQDVASAFEPNNENWERNLAEKEDNVKSYNDMQRASPDLSITGYMLSPQYKIPCLFEDV 300
Qy      1007  NDIDVQGMLEILMTYFSAQRIELHLNHSQFIESIRPALLESKASVTKCSISKLELS 1066
Db      301  NDIDVQGMLEILMTYFSAQRIELHLNHSQFIESIRPALLESKASVTKCSISKLELS 1066
Qy      1067  AAQOELLTLPSLESLEVSQTIQSQ 1091
Db      361  AAQOELLTLPSLESLEVSQTIQSQ 365

```

## RESULT 7

```

US-10-029-386-33933
; Sequence 33933, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33933
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005031.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALUATION 1.00e-112
US-10-029-386-33933

```

```

Query Match      14.5%; Score 203; DB 12; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.2e-186;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      389  MAGGEQWQOEAKNLEQLRAAYTSAPRHSILDISDLATDHLGCDLSISKHISKP 448
Db      1  MAGGEQWQOEAKNLEQLRAAYTSAPRHSILDISDLATDHLGCDLSISKHISKP 60
Qy      449  VQEPVLPFVFNLSVNCVGEAGSGKTVLLKIAFLMASGCCPLNRFQVLYSTLS 508
Db      61  VQEPVLPFVFNLSVNCVGEAGSGKTVLLKIAFLMASGCCPLNRFQVLYSTLS 120
Qy      509  TRPDGLASIIICDQLEKEGSTEKMKNNIIQQKNOVFLLDYKEIGSPIVIGKLIQ 568
Db      121  TRPDGLASIIICDQLEKEGSTEKMKNNIIQQKNOVFLLDYKEIGSPIVIGKLIQ 180
Qy      569  KNLHSLRTCLLAVATNRADIR 591
Db      181  KNLHSLRTCLLAVATNRADIR 203

```

## RESULT 8

```

US-09-925-299-1033
; Sequence 1033, Application US/09925299

```

```

; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1033
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1033

```

```

Query Match      5.3%; Score 75; DB 9; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.2e-63;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      607  TVCILRLFSHNTRLRKFMVYFGKQSLQKTKTPLFVAALCAHWFOYPPDPSFDDVAV 666
Db      1  TVCILRLFSHNTRLRKFMVYFGKQSLQKTKTPLFVAALCAHWFOYPPDPSFDDVAV 60
Qy      667  FKSIMERLSLRNKAT 681
Db      61  FKSIMERLSLRNKAT 75

```

## RESULT 9

```

US-09-925-299-1033
; Sequence 1033, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1033
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1033

```

```

Query Match      5.3%; Score 75; DB 11; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.2e-63;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      607  TVCILRLFSHNTRLRKFMVYFGKQSLQKTKTPLFVAALCAHWFOYPPDPSFDDVAV 666
Db      1  TVCILRLFSHNTRLRKFMVYFGKQSLQKTKTPLFVAALCAHWFOYPPDPSFDDVAV 60
Qy      667  FKSIMERLSLRNKAT 681
Db      61  FKSIMERLSLRNKAT 75

```

## RESULT 10

```

US-10-138-618-26
; Sequence 26, Application US/10138618
; Publication No. US20030100525A1
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.

```

TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,618  
FILING DATE: 06-May-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/975,080  
FILING DATE: 20-NOV-1997  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-10-138-618-26

Query Match 3.6%; Score 50; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6,5e-40;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 YTGKIDIVQCFSCGCGCLEKMQEGBDPLDHTRCPPNCPFLQNMKSSAEVT 355  
Db 1 YTGKIDIVQCFSCGCGCLEKMQEGBDPLDHTRCPPNCPFLQNMKSSAEVT 50

RESULT 11  
US-10-138-618-13  
Sequence 13, Application US/10138618  
Publication No. US20030100525A1  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,618  
FILING DATE: 06-May-2002

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/975,080  
FILING DATE: 20-NOV-1997  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 47 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-138-618-13

Query Match 3.3%; Score 47; DB 15; Length 47;  
Best Local Similarity 100.0%; Pred. No. 4.8e-37;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 EEARLASFRWPFYVQGISPCVLSBAGFVPTGKODIVQCFSCGCGCIG 205  
Db 1 EEARLASFRWPFYVQGISPCVLSBAGFVPTGKODIVQCFSCGCGCIG 47

RESULT 12  
US-09-864-761-47337  
Sequence 47337, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47337
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005031.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.55
; OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALU8 5.00e-06
; OTHER INFORMATION: EST_HUMAN HIT: AA358493.1, EVALU8 1.00e-13
; US-09-864-761-47337

Query Match
Best Local Similarity 1.6%; Score 22; DB 9; Length 37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 SKKSEETIYIYISYKGFVDIT 250
DB 1 SKKSEETIYIYISYKGFVDIT 22

RESULT 13
US-09-841-739-11
; Sequence 11, Application US/09841739
; Patent No. US20030034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
; US-09-841-739-11

Query Match
Best Local Similarity 0.9%; Score 12; DB 9; Length 898;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 OKTPLFVAALCA 650
DB 193 OKTPLFVAALCA 204

RESULT 14
US-10-449-315-11
; Sequence 11, Application US/10449315
; Publication No. US20030190679A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
```

```

; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
; US-10-449-315-11

Query Match
Best Local Similarity 0.9%; Score 12; DB 12; Length 898;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 OKTPLFVAALCA 650
DB 193 OKTPLFVAALCA 204

RESULT 15
US-09-812-471-20
; Sequence 20, Application US/09812471
; Patent No. US20020018765A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/062802
; CURRENT APPLICATION NUMBER: US/09/812,471
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
; US-09-812-471-20

Query Match
Best Local Similarity 0.6%; Score 8; DB 9; Length 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPLD 333
DB 3 QEGDDPLD 10

RESULT 16
US-09-812-633-20
; Sequence 20, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, David
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
```



;; CURRENT APPLICATION NUMBER: US/09/812,633  
;; CURRENT FILING DATE: 2001-03-19  
;; PRIOR APPLICATION NUMBER: US 60/216,723  
;; PRIOR FILING DATE: 2000-07-07  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 20  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: derived from Polyoma virus large T antigen  
US-09-812-633-20

Query Match 0.6%; Score 8; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPLD 333  
Db 3 QEGDDPLD 10

RESULT 17  
US-09-988-117-20  
;; Sequence 20, Application US/09988117  
;; Patent No. US20020156039A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Benjamin, Thomas L.  
;; APPLICANT: Li, Dawei  
;; APPLICANT: Mok, Samuel C.  
;; APPLICANT: Cramer, Daniel W.  
;; APPLICANT: Ma, Yupo  
;; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
;; TITLE OF INVENTION: Using Sal2  
;; FILE REFERENCE: 00742/066002  
;; CURRENT APPLICATION NUMBER: US/09/988,117  
;; CURRENT FILING DATE: 2001-11-16  
;; PRIOR APPLICATION NUMBER: US 09/812,633  
;; PRIOR FILING DATE: 2001-03-19  
;; PRIOR APPLICATION NUMBER: US 60/216,723  
;; PRIOR FILING DATE: 2000-07-07  
;; NUMBER OF SEQ ID NOS: 21  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 20  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: derived from Polyoma virus large T antigen  
US-09-988-117-20

Query Match 0.6%; Score 8; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPLD 333  
Db 3 QEGDDPLD 10

RESULT 18  
US-09-933-767-580  
;; Sequence 580, Application US/09933767  
;; Publication No. US20030181692A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ni et al.  
;; TITLE OF INVENTION: 207 Human Secreted Proteins  
;; FILE REFERENCE: P2007P2  
;; CURRENT APPLICATION NUMBER: US/09/933,767  
;; CURRENT FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: PCT/US01/05614  
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: 60/184,836  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: 60/193,170  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: 09/205,258  
;; PRIOR FILING DATE: 1998-12-04  
;; PRIOR APPLICATION NUMBER: PCT/US98/11422  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/048,885  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/049,375  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/048,881  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/048,880  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/048,896  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/049,020  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/048,876  
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;; PRIOR APPLICATION NUMBER: 60/048,962

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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048, 963
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; PRIOR APPLICATION NUMBER: 60/048, 878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068, 054
; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1997-12-18
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; PRIOR APPLICATION NUMBER: 60/073, 165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073, 164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085, 925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085, 921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085, 923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085, 922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092, 921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094, 657
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 580
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-767-580

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Query Match      0.64; Score 8; DB 12; Length 64;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 39 EEEEXKER 46
Db 29 EEEEXKER 36

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RESULT 19
US-10-023-282-580
; Sequence 580, Application US/1002282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023, 282
; EARLIER FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205, 258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048, 885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 880

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; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049, 020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 894
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; EARLIER APPLICATION NUMBER: 60/049, 019
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048, 878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070, 923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092, 921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094, 657
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0

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SEQ ID NO 580  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-282-580

Query Match  
Best Local Similarity 100.0%; Score 8; DB 15; Length 64;  
Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEQKKER 46  
Db 29 EEEQKKER 36

RESULT 20  
US-09-201-936-16  
Sequence 16, Application US/09201936  
Publication No. US20020187946A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Baird, Stephen  
APPLICANT: Liston, Peter  
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
FILE REFERENCE: 07891/003003  
CURRENT APPLICATION NUMBER: US/09/201,936  
CURRENT FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/011,356  
EARLIER FILING DATE: 1998-02-04  
EARLIER APPLICATION NUMBER: PCT/IB96/01022  
EARLIER FILING DATE: 1996-08-05  
EARLIER APPLICATION NUMBER: 08/576,956  
EARLIER FILING DATE: 1995-12-22  
EARLIER APPLICATION NUMBER: 08/511,485  
EARLIER FILING DATE: 1995-08-04  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 16  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-201-936-16

Query Match  
Best Local Similarity 100.0%; Score 8; DB 10; Length 68;  
Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DTVCFCSC 200  
Db 34 DTVCFCSC 41

RESULT 21  
US-09-925-297-743  
Sequence 743, Application US/09925297  
Patent No. US20020081659A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA105  
CURRENT APPLICATION NUMBER: US/09/925,297  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05989  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 928  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 743  
LENGTH: 95  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: 1(4)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-297-743

Query Match  
Best Local Similarity 100.0%; Score 8; DB 9; Length 95;  
Pred. No. 31;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 EKLLIQIS 1139  
Db 37 EKLLIQIS 44

RESULT 22  
US-10-156-761-8837  
Sequence 8837, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIRAMA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 8837  
LENGTH: 201  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-8837

Query Match  
Best Local Similarity 100.0%; Score 8; DB 15; Length 201;  
Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 SAEVTPDL 358  
Db 33 SAEVTPDL 40

RESULT 23  
US-09-925-299-821  
Sequence 821, Application US/09925299  
Patent No. US20020055627A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA102  
CURRENT APPLICATION NUMBER: US/09/925,299  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05883  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1556  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 821  
LENGTH: 259  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-299-821

Query Match  
Best Local Similarity 0.6%; Score 8; DB 9; Length 259;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 39 EEEBOKER 46  
174 EEEBOKER 181

## RESULT 24

US-09-925-299-821  
; Sequence 821, Application US/09925299  
; Publication No. US2003040617A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA102  
; CURRENT APPLICATION NUMBER: US/09/925,299  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05883  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; NUMBER OF SEQ ID NOS: 1556  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 821  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-299-821

Query Match  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 39 EEEBOKER 46  
174 EEEBOKER 181

## RESULT 25

US-10-156-761-12012  
; Sequence 12012, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 12012  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-12012

Query Match  
Best Local Similarity 0.6%; Score 8; DB 15; Length 481;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

293 AVGVALA 300

DB 9 AVGVALA 16

## RESULT 26

US-09-974-592-10  
; Sequence 10, Application US/09974592  
; Patent No. US20020120121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Teang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009004  
; CURRENT APPLICATION NUMBER: US/09/974,592  
; PRIOR FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-974-592-10

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 193 DTVOCFSC 200  
59 DTVOCFSC 66

## RESULT 27

US-09-201-936-10  
; Sequence 10, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; PRIOR FILING DATE: 1998-12-01  
; PRIOR APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-201-936-10

Query Match  
Best Local Similarity 0.6%; Score 8; DB 10; Length 496;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 DTWCFCSC 200  
Db 59 DTWCFCSC 66

## RESULT 28

US-09-933-767-573  
; Sequence 573, Application US/09933767  
; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
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; PRIOR APPLICATION NUMBER: 60/049,374  
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; PRIOR APPLICATION NUMBER: 60/048,974  
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; PRIOR APPLICATION NUMBER: 60/048,883  
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; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 573  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (409)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-933-767-573

Query Match 0.64; Score 8; DB 12; Length 567;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 39 EEEBOKER 46  
|||||

Db 483 EEEBOKER 490

RESULT 29  
US-10-023-282-573  
Sequence 573, Application US/10023282  
Publication No. US20030092893A1  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT FILING DATE: US/10/023, 282  
EARLIER APPLICATION NUMBER: 2001-12-20  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048, 885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049, 374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 949  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048, 974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048, 876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070, 923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092, 921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094, 657  
EARLIER FILING DATE: 1998-07-30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 573  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (409)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-023-282-573

Query Match  
Best Local Similarity 0.6%; Score 8; DB 15; Length 567;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 483 EEEBOKER 490

RESULT 30  
US-09-896-852-55  
Sequence 55, Application US/09896852  
Patent No. US20020025542A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Maine, Gregory T.  
APPLICANT: Hunt, Jeffrey C.  
APPLICANT: Brojanec, Susan  
APPLICANT: Jhy-Tsing Sheu, Michael  
APPLICANT: Chovan, Linda E.  
APPLICANT: Tyner, Joan D.  
TITLE OF INVENTION: ANTIGEN COCKTAILS, P35, AND USES THEREOF  
FILE REFERENCE: 6361.US.D1  
CURRENT FILING DATE: US/09/896, 852  
PRIOR APPLICATION NUMBER: 2001-06-29  
PRIOR FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 55  
LENGTH: 667  
TYPE: PRT  
ORGANISM: Toxoplasma gondii  
US-09-896-852-55

Query Match  
Best Local Similarity 0.6%; Score 8; DB 9; Length 667;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
Db 542 FGAGLTRL 549

## RESULT 31

US-09-728-644-55  
; Sequence 55, Application US/09728644  
; Publication No. US20030119053A1  
; GENERAL INFORMATION:  
; APPLICANT: MAINE, Gregory T.  
; APPLICANT: HUNT, Jeffrey C.  
; APPLICANT: BROJANAC, Susan  
; APPLICANT: JYH-TSING SHEU, Michael  
; APPLICANT: CHOYAN, Linda E.  
; APPLICANT: TYNER, Joan D.  
; APPLICANT: HOWARD, Lawrence V.  
; APPLICANT: PARMLEY, Stephen F.  
; APPLICANT: REMINGTON, Jack S.  
; APPLICANT: ARAUJO, Fausto  
; APPLICANT: SUZUKI, Yasuhiko  
; APPLICANT: LI, Shuli  
; TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF  
; FILE REFERENCE: 6361.US.P1  
; CURRENT APPLICATION NUMBER: US/09/728,644  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/303,064  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 667  
; TYPE: PRT  
; ORGANISM: Toxoplasma gondii  
US-09-728-644-55

Query Match 0.6%; Score 8; DB 11; Length 667;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FGAGLTRL 112  
Db 542 FGAGLTRL 549

## RESULT 32

US-09-969-528-2  
; Sequence 2, Application US/09969528  
; Patent No. US20020150567A1  
; GENERAL INFORMATION:  
; APPLICANT: POT, David A.  
; APPLICANT: WILLIAMS, Lewis T.  
; APPLICANT: JEFFERSON, Anne Bennett  
; APPLICANT: MAJERUS, Philip W.  
; TITLE OF INVENTION: No. US20020150567A1e1 Grb2 Associating Protein and Nucleic  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/969,528  
; FILING DATE: 01-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/560,005

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307K-0624000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 976 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-969-528-2

Query Match 0.6%; Score 8; DB 10; Length 976;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1075 TLPSLSSL 1082  
Db 14 TLPSLSSL 21

## RESULT 33

US-10-291-607-15  
; Sequence 15, Application US/10291607  
; Publication No. US20030143232A1  
; GENERAL INFORMATION:  
; APPLICANT: Altieri, Dario C.  
; TITLE OF INVENTION: Methods for Selectively Modulating Survivalin Apoptosis  
; FILE REFERENCE: 44574-5063-US  
; CURRENT APPLICATION NUMBER: US/10/291,607  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: US/09/515,514  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: NADP phosphorylation motif  
US-10-291-607-15

Query Match 0.5%; Score 7; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.2e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 WIPOEWA 82  
Db 1 WIPOEWA 7

## RESULT 34

US-09-812-471-15  
; Sequence 15, Application US/09812471  
; Patent No. US20020018765A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Thomas L.  
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
; FILE REFERENCE: 00742/062002  
; CURRENT APPLICATION NUMBER: US/09/812,471  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: US 60/216,723

```

; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-471-15

```

```

Query Match      0.5%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      326 QEGDDPL 332
DB      3 QEGDDPL 9

```

```

RESULT 35
US-09-812-633-15
; Sequence 15, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
; CURRENT APPLICATION NUMBER: US/09/812,633
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-633-15

```

```

Query Match      0.5%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      326 QEGDDPL 332
DB      3 QEGDDPL 9

```

```

RESULT 36
US-09-988-117-15
; Sequence 15, Application US/09988117
; Patent No. US20020156039A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066002
; CURRENT APPLICATION NUMBER: US/09/988,117
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/812,633
; PRIOR FILING DATE: 2001-03-19

```

```

; PRIOR APPLICATION NUMBER: US 60/216,723
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-988-117-15

```

```

Query Match      0.5%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      326 QEGDDPL 332
DB      3 QEGDDPL 9

```

```

RESULT 37
US-09-812-471-14
; Sequence 14, Application US/09812471
; Patent No. US2002018765A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/062002
; CURRENT APPLICATION NUMBER: US/09/812,471
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: derived from Polyoma virus large T antigen
US-09-812-471-14

```

```

Query Match      0.5%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      326 QEGDDPL 332
DB      3 QEGDDPL 9

```

```

RESULT 38
US-09-812-633-14
; Sequence 14, Application US/09812633
; Patent No. US20020147996A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Thomas L.
; APPLICANT: Li, Dawei
; APPLICANT: Mok, Samuel C.
; APPLICANT: Cramer, Daniel W.
; APPLICANT: Ma, Yupo
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells
; FILE REFERENCE: 00742/066001
; CURRENT APPLICATION NUMBER: US/09/812,633
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: US 60/216,723
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14

```



LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: derived from Polyoma virus large T antigen  
US-09-812-633-14

Query Match 0.5%; Score 7; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332  
Db 3 QEGDDPL 9

RESULT 39  
US-09-988-117-14  
Sequence 14, Application US/09988117  
Patent No. US20020156039A1  
GENERAL INFORMATION:  
APPLICANT: Benjamin, Thomas L.  
APPLICANT: Li, Dawei  
APPLICANT: Mok, Samuel C.  
APPLICANT: Cramer, Daniel W.  
APPLICANT: Ma, Yupo  
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
FILE REFERENCE: 00742/066002  
CURRENT APPLICATION NUMBER: US/09/988,117  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: US 09/812,633  
PRIOR FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: US 60/216,723  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: derived from Polyoma virus large T antigen  
US-09-988-117-14

Query Match 0.5%; Score 7; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332  
Db 3 QEGDDPL 9

RESULT 40  
US-09-812-471-13  
Sequence 13, Application US/09812471  
Patent No. US2002018765A1  
GENERAL INFORMATION:  
APPLICANT: Benjamin, Thomas L.  
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
FILE REFERENCE: 00742/066002  
CURRENT APPLICATION NUMBER: US/09/812,471  
CURRENT FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: US 60/216,723  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Polyoma virus

US-09-812-471-13  
Query Match 0.5%; Score 7; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332  
Db 3 QEGDDPL 9

RESULT 41  
US-09-812-633-13  
Sequence 13, Application US/09812633  
Patent No. US20020147996A1  
GENERAL INFORMATION:  
APPLICANT: Benjamin, Thomas L.  
APPLICANT: Li, Dawei  
APPLICANT: Mok, Samuel C.  
APPLICANT: Cramer, Daniel W.  
APPLICANT: Ma, Yupo  
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
FILE REFERENCE: 00742/066001  
CURRENT APPLICATION NUMBER: US/09/812,633  
CURRENT FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: US 60/216,723  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Polyoma virus  
US-09-812-633-13

Query Match 0.5%; Score 7; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 QEGDDPL 332  
Db 3 QEGDDPL 9

RESULT 42  
US-09-988-117-13  
Sequence 13, Application US/09988117  
Patent No. US20020156039A1  
GENERAL INFORMATION:  
APPLICANT: Benjamin, Thomas L.  
APPLICANT: Li, Dawei  
APPLICANT: Mok, Samuel C.  
APPLICANT: Cramer, Daniel W.  
APPLICANT: Ma, Yupo  
TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
FILE REFERENCE: 00742/066002  
CURRENT APPLICATION NUMBER: US/09/988,117  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: US 09/812,633  
PRIOR FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: US 60/216,723  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Polyoma virus  
US-09-988-117-13

Query Match 0.5%; Score 7; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 QEGDDPL 332  
Db 3 QEGDDPL 9

## RESULT 43

US-09-812-471-10  
; Sequence 10, Application US/09812471  
; Patent No. US20020018765A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Thomas L.  
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
; FILE REFERENCE: 00742/062002  
; CURRENT APPLICATION NUMBER: US/09/812,471  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: US 60/216,723  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Polyoma virus  
US-09-812-471-10

## Query Match

Best Local Similarity 0.5%; Score 7; DB 9; Length 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 QEGDDPL 332  
Db 7 QEGDDPL 13

## RESULT 44

US-09-812-633-10  
; Sequence 10, Application US/09812633  
; Patent No. US20020147996A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Thomas L.  
; APPLICANT: Li, Dawei  
; APPLICANT: Mok, Samuel C.  
; APPLICANT: Cramer, Daniel W.  
; APPLICANT: Ma, Yupo  
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
; FILE REFERENCE: 00742/066001  
; CURRENT APPLICATION NUMBER: US/09/812,633  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: US 60/216,723  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Polyoma virus  
US-09-812-633-10

Query Match 0.5%; Score 7; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 QEGDDPL 332  
Db 7 QEGDDPL 13

## RESULT 45

US-09-988-117-10  
; Sequence 10, Application US/09988117  
; Patent No. US20020156039A1  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Thomas L.  
; APPLICANT: Li, Dawei  
; APPLICANT: Mok, Samuel C.  
; APPLICANT: Cramer, Daniel W.  
; APPLICANT: Ma, Yupo  
; TITLE OF INVENTION: Diagnosing and Treating Cancer Cells  
; FILE REFERENCE: 00742/066002  
; CURRENT APPLICATION NUMBER: US/09/988,117  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/812,633  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: US 60/216,723  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Polyoma virus  
US-09-988-117-10

## Query Match

Best Local Similarity 0.5%; Score 7; DB 10; Length 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 QEGDDPL 332  
Db 7 QEGDDPL 13

## RESULT 46

US-09-726-643-145  
; Sequence 145, Application US/09726643  
; Patent No. US20020028449A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 26 Human secreted proteins  
; FILE REFERENCE: P20404p1  
; CURRENT APPLICATION NUMBER: US/09/726,643  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/15187  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,725  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.0  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-726-643-145

Query Match 0.5%; Score 7; DB 9; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1,44+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1340 ATTIVKSL 1346  
Db 13 ATTIVKSL 19

## RESULT 47

US-10-042-141-145  
; Sequence 145, Application US/10042141  
; Publication No. US20020183503A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 26 Human secreted proteins

FILE REFERENCE: P2040P1  
CURRENT APPLICATION NUMBER: US/10/042,141  
CURRENT FILING DATE: 2002-01-11  
PRIOR APPLICATION NUMBER: 09/726,643  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/15187  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/137,725  
PRIOR FILING DATE: 1999-06-07  
NUMBER OF SEQ ID NOS: 190  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 145  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-042-141-145

Query Match 0.5%; Score 7; DB 14; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1340 ATTAKSL 1346  
DB 13 ATTAKSL 19

RESULT 48  
US-10-232-286-9  
Sequence 9, Application US/10232286  
Publication No. US20030143579A1  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/232,286  
FILING DATE: 30-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-232-286-9

Query Match 0.5%; Score 7; DB 12; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAAMP 222  
DB 39 EHAAMP 45

RESULT 49  
US-09-071-838-94  
Sequence 94, Application US/09071838  
Patent No. US20020152501A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramon  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: Nucleic Acids That Control Seed and  
TITLE OF INVENTION: Fruit Development in Plants  
NUMBER OF SEQUENCES: 324  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,838  
FILING DATE: 01-MAY-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-086100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-071-838-94

Query Match 0.5%; Score 7; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 RLKRFV 627  
DB 20 RLKRFV 26

RESULT 50  
US-10-138-618-21  
Sequence 21, Application US/10138618  
Publication No. US20030100525A1  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,618  
FILING DATE: 06-May-2002  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/975,080  
FILING DATE: 20-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-10-138-618-21

Query Match 0.5%; Score 7; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKEP 222  
Db 29 EHAKEP 35

RESULT 51  
US-10-138-618-22  
Sequence 22, Application US/10138618  
Publication No. US20030100525A1  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,618  
FILING DATE: 06-May-2002  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/975,080  
FILING DATE: 20-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-138-618-31

ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-10-138-618-22

Query Match 0.5%; Score 7; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 EHAKEP 222  
Db 29 EHAKEP 35

RESULT 52  
US-10-138-618-31  
Sequence 31, Application US/10138618  
Publication No. US20030100525A1  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,618  
FILING DATE: 06-May-2002  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/975,080  
FILING DATE: 20-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-138-618-31

Query Match 0.5%; Score 7; DB 15; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 EHAKEFP 222  
DB 29 EHAKEFP 35

## RESULT 53

US-10-213-512-94  
Sequence 94, Application US/10213512  
Publication No. US20030110536A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Fruit Development in Plants  
FILE REFERENCE: 023070-08611005  
CURRENT APPLICATION NUMBER: US/10/213,512  
CURRENT FILING DATE: 2002-08-06  
PRIOR APPLICATION NUMBER: US/09/177,206  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: US 09/071,838  
PRIOR FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 94  
LENGTH: 50  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-10-213-512-94

Query Match 0.5%; Score 7; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 RLKRFV 627  
DB 20 RLKRFV 26

## RESULT 54

US-09-864-761-43582  
Sequence 43582, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine ver. 1.1

SEQ ID NO 43582

LENGTH: 52

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC004123.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.63

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75

US-09-864-761-43582

Query Match 0.5%; Score 7; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEEOKE 45  
DB 11 EEEEOKE 17

## RESULT 55

US-09-864-761-47236  
Sequence 47236, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30

```

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47236
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003049.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63
US-09-864-761-47236

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```

Query Match
Best Local Similarity 0.5%; Score 7; DB 9; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 39 EEEEOKE 45
Db 15 EEEEOKE 21

```

```

RESULT 56
US-10-156-761-8279
; Sequence 8279, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8279
; LENGTH: 56

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```

; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8279

```

```

Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 102 LILFGAG 108
Db 12 LILFGAG 18

```

```

RESULT 57
US-10-156-761-8496
; Sequence 8496, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8496
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8496

```

```

Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 102 LILFGAG 108
Db 12 LILFGAG 18

```

```

RESULT 58
US-09-864-761-46549
; Sequence 46549, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46549
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078461.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q61687, EVALUATE 3.40e-02
; OTHER INFORMATION: EST_HUMAN HIT: AF114027.1, EVALUATE 1.00e-30
; US-09-864-761-46549
; Query Match 0.5%; Score 7; DB 9; Length 64;
; Best Local Similarity 100.0%; Pred. No. 2e+02;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 822 ENISEND 828
; DB 17 ENISEND 23
;
; RESULT 59
; US-09-864-761-43318
; Sequence 43318, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT FILING DATE: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43318
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004123.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: R60198.1, EVALUATE 5.70e+00
; OTHER INFORMATION: SWISSPROT HIT: P03518, EVALUATE 5.90e+00
; US-09-864-761-43318
; Query Match 0.5%; Score 7; DB 9; Length 66;
; Best Local Similarity 100.0%; Pred. No. 2.1e+02;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1205 FISLKITL 1211
; DB 22 FISLKITL 28
;
; RESULT 60
; US-09-201-936-23
; Sequence 23, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: PROBES, AND DETECTION METHODS
; CURRENT FILING DATE: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356

```

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; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-23

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Query Match
Best Local Similarity 0.5%; Score 7; DB 10; Length 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 339 FPCPPL 345
DB 61 FPCPPL 67

```

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RESULT 61
US-09-201-936-27
; Sequence 27, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 27
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-27

```

```

Query Match
Best Local Similarity 0.5%; Score 7; DB 10; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 BHAKWP 222
DB 57 BHAKWP 63

```

```

RESULT 62
US-10-041-859-15
; Sequence 15, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND

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; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; EARLIER FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 15
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
US-10-041-859-15

```

```

Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 284 SFDWPR 290
DB 7 SFDWPR 13

```

```

RESULT 63
US-10-041-859-16
; Sequence 16, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; EARLIER FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 16
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Trichoplusia ni
US-10-041-859-16

```

```

Query Match
Best Local Similarity 0.5%; Score 7; DB 15; Length 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 284 SFDWPR 290
DB 7 SFDWPR 13

```

```

RESULT 64
US-09-864-761-44802
; Sequence 44802, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; EARLIER FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456

```



PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 44802  
LENGTH: 69  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC025516.2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87  
OTHER INFORMATION: SWISSPROT HIT: Q9WUQ1, EVALU8 4.00e-07  
OTHER INFORMATION: EST\_HUMAN HIT: AW501874.1, EVALU8 4.20e+00  
US-09-864-761-44802

Query Match 0.5%; Score 7; DB 9; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1374 LNWKER 1380  
Db 5 LNWKER 11

RESULT 65  
US-10-106-698-4757  
Sequence 4757, Application US/10106698  
Publication No. US20030109690A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
FILE REFERENCE: PA005P1  
CURRENT APPLICATION NUMBER: US/10/106,698  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: PCT/US00/26524  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: US 60/163,280  
PRIOR FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 8564  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 4757  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-106-698-4757

Query Match 0.5%; Score 7; DB 15; Length 84;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1073 LTLPLS 1079  
Db 20 LTLPLS 26

RESULT 66  
US-10-029-386-30446  
Sequence 30446, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 30446  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR22.124.0  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.8  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66  
OTHER INFORMATION: SWISSPROT HIT: P36151, EVALU8 6.00e-03  
US-10-029-386-30446

Query Match 0.5%; Score 7; DB 12; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ELSALG 28  
Db 60 ELSALG 66

RESULT 67  
US-09-864-761-38254  
Sequence 38254, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04

```

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38254
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010680.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EST HUMAN HIT: P35989.1, EVALU 1.00e-23
US-09-864-761-38254

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Query Match      0.5% Score 7; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      857 SWVSEHL 863
DB      50 SWVSEHL 56

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RESULT 68

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; Sequence 34814, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AccuCa-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04

```

```

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34814
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006946.18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EST HUMAN HIT: BE280799.1, EVALU 1.00e-32
US-09-864-761-34814

```

```

Query Match      0.5% Score 7; DB 9; Length 101;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      22 ELSSALG 28
DB      60 ELSSALG 66

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RESULT 69

```

```

; Sequence 39550, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

```

```

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39550
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004752.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: SWISSPROT HIT: P18168, EVALUATE 4.60e+00
US-09-864-761-39550
Query Match 0.5%; Score 7; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 RLRKENV 627
|||||
Db 4 RLRKENV 10

```

```

; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMTA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8010
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Streptomyces avermiltilis
US-10-156-761-8010

Query Match          0.5%; Score 7; DB 15; Length 107;
Best Local Similarity 100.0%; Pred.No.3.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      293 AVGVNALL 299
      |||||
Db      32 AVGVNALL 38

RESULT 71
US-09-867-550-1404
; Sequence 1404, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1404
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-1404

Query Match          0.5%; Score 7; DB 9; Length 109;
Best Local Similarity 100.0%; Pred.No.3.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1237 LEEILIP 1243
      |||||
Db      36 LEEILIP 42

RESULT 72
US-10-029-386-32489
; Sequence 32489, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.

```

```

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32489
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132642.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P48187, EVALU 1.30e+00
US-10-029-386-32489
```

## Query Match

Best Local Similarity 0.5%; Score 7; DB 12; Length 130;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1263 HCLRVLS 1269
DB      89 HCLRVLS 95
```

## RESULT 73

```

US-10-287-274-415
; Sequence 415, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlgen, Karl
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY
; FILE REFERENCE: ELITRA.008DV1
; CURRENT APPLICATION NUMBER: US/10/287,274
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 415
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-415
```

## Query Match

Best Local Similarity 0.5%; Score 7; DB 12; Length 134;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      19 LLPELSA 25
DB      86 LLPELSA 92
```

## RESULT 74

```

US-09-815-242-5364
; Sequence 5364, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlgen, Karl L.
; APPLICANT: Zykkind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
```

```

; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; NUMBER OF SEQ ID NOS: 60/191,078
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32489
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132642.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: SWISSPROT HIT: P48187, EVALU 1.30e+00
US-10-029-386-32489
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## Query Match

Best Local Similarity 0.5%; Score 7; DB 9; Length 139;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1060 ISKLELS 1066
DB      95 ISKLELS 91
```

## RESULT 75

```

US-10-156-761-14388
; Sequence 14388, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: Ohtsuka, Satoshi
; APPLICANT: Iweda, Haruo
; APPLICANT: Ishikawa, Jun
; APPLICANT: Horikawa, Hiroshi
; APPLICANT: Shiba, Tadayoshi
; APPLICANT: Sakaki, Yoshiyuki
; APPLICANT: Hattori, Masahira
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14388
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14388
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## Query Match

Best Local Similarity 0.5%; Score 7; DB 15; Length 144;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      31 AVOLAKE 37
DB      109 AVOLAKE 115
```

Thu Dec 18 09:31:08 2003

us-09-830-338-1.oligo.rapb

Page 29

Search completed: December 18, 2003, 09:26:17  
Job time : 288 secs

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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 18, 2003, 09:11:49 ; Search time 60 Seconds  
(without alignments)  
3711.556 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 1403  
Sequence: 1 MATQKASDERISQFDHNL.....SKYLTILQKWLFPSPRIQK 1403

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403	100.0	1403	AAW20032	Neuronal apoptosis
2	1403	100.0	1403	AAV14079	Neurotrophic factor
3	1403	100.0	1403	AAV09539	Human apoptosis in
4	1403	100.0	1403	AAV88053	Human NAIP protein
5	1403	100.0	1403	ABR72166	Human inhibitor of
6	1403	100.0	1403	ABU07400	Protein different
7	1282	91.4	1295	AAV14080	Neurotrophic factor
8	1282	91.4	1295	AAV09540	Human apoptosis in
9	1064	77.3	1403	AAW20033	Neuronal apoptosis

10	946	67.4	1232	17	AA898217	Neuronal apoptosis
11	75	5.3	118	21	AA853493	Human colon cancer
12	60	4.3	60	21	AA801849	Human secreted pro
13	25	1.8	51	28	AA012411	Human polypeptide
14	22	1.6	37	22	ABG55972	Human liver peptid
15	22	1.6	37	22	AAW74180	Human bone marrow
16	22	1.6	37	22	AAW34307	Human peptide enco
17	22	1.6	37	22	ABG44119	Human polypeptide
18	22	1.6	37	22	AA006778	Streptococcus pneu
19	9	0.6	210	24	ABP81447	S. pneumoniae type
20	9	0.6	210	24	ABU02180	Arabidopsis thalia
21	9	0.6	341	21	AA828074	Novel protein kina
22	9	0.6	349	22	AA865694	Human protein kina
23	23	0.6	350	22	AAU03542	Human polypeptide
24	9	0.6	350	23	ABP69792	Arabidopsis thalia
25	9	0.6	466	21	AA828072	Arabidopsis thalia
26	9	0.6	466	21	AA828072	Arabidopsis thalia
27	27	0.6	15	23	AAE17965	Polyoma virus larg
28	8	0.6	56	22	AA83576	Human immune/haema
29	8	0.6	64	22	AA850632	Human secreted pro
30	30	0.6	95	21	AA854291	Human pancreatic c
31	8	0.6	113	22	AAU42144	Propionibacterium
32	8	0.6	152	21	AA807152	Arabidopsis thalia
33	8	0.6	152	21	AA835555	Arabidopsis thalia
34	8	0.6	197	22	AA866125	Drosophila melanog
35	8	0.6	232	21	AA807151	Arabidopsis thalia
36	8	0.6	232	21	AA853554	Arabidopsis thalia
37	8	0.6	239	21	AA807150	Arabidopsis thalia
38	8	0.6	239	21	AA853553	Arabidopsis thalia
39	8	0.6	259	21	AA853281	Human colon cancer
40	8	0.6	358	21	AA807235	Arabidopsis thalia
41	8	0.6	358	21	AA848600	Arabidopsis thalia
42	8	0.6	358	23	AB892886	Herbicidally activ
43	8	0.6	373	21	AA848599	Arabidopsis thalia
44	8	0.6	374	21	AA807234	Arabidopsis thalia
45	8	0.6	428	12	AA813552	Toxoplasma gondii
46	8	0.6	441	20	AA834752	Chlamydia pneumonia
47	8	0.6	496	18	AAW19745	Mouse inhibitor of
48	8	0.6	496	18	AAW19584	Mouse apoptosis in
49	8	0.6	496	19	AAW62927	Mouse apoptosis in
50	8	0.6	496	24	ABG65666	Mouse inhibitor of
51	8	0.6	496	24	ABG72157	Mouse inhibitor of
52	8	0.6	506	23	ABP41530	Human ovarian anti
53	8	0.6	519	22	ABG09940	Novel human diagno
54	8	0.6	521	22	AB841920	Drosophila melanog
55	8	0.6	523	15	AA871976	Pertussis A. Bord
56	8	0.6	538	22	AB867078	Drosophila melanog
57	8	0.6	567	22	AAW88788	Polypeptide fragme
58	8	0.6	567	22	AB850625	Human secreted pro
59	8	0.6	568	21	AAW85658	Human Actinus S' pr
60	8	0.6	575	22	AB871239	Drosophila melanog
61	8	0.6	583	21	AAW85659	Human Actinus S' pr
62	8	0.6	614	22	ABG09939	Novel human diagno
63	8	0.6	654	21	AAW57754	CKS-P66-CKS fusion
64	8	0.6	679	22	AB871989	Drosophila melanog
65	8	0.6	845	22	AAW79222	Amino acid sequenc
66	8	0.6	848	23	ABG66688	Human novel polype
67	8	0.6	906	23	ABG66687	Human novel polype
68	8	0.6	934	23	AB891916	Herbicidally activ
69	8	0.6	968	18	AAW21721	SH2-A. Homo sapie
70	8	0.6	976	18	AAW26624	Signalling inositol
71	8	0.6	976	18	AAW18327	BRB2 associating p
72	8	0.6	1187	18	AAW14002	Mouse SH2-containi
73	8	0.6	1187	18	AAW14003	Human SH2-containi
74	8	0.6	1189	18	AAW26623	Signalling inositol
75	8	0.6	1341	21	AAW85657	Human Actinus L pro
76	8	0.6	1342	22	ABG09943	Novel human diagno
77	8	0.6	2097	22	ABG09944	Novel human diagno
78	7	0.5	7	22	AAW45906	H11 binding site c
79	7	0.5	7	22	AAW45911	H11 binding site c
80	7	0.5	7	22	AAW45916	H11 binding site c
81	7	0.5	10	23	AAE17960	Polyoma virus larg
82	7	0.5	14	23	AAE17959	Polyoma virus larg





QY 1021 MTFVFSASQRIEHLNHSRGFISIRPALELSKASVTKCSISKLELSAEOELLTLPSLE 1080  
 DB 1021 MTFVFSASQRIEHLNHSRGFISIRPALELSKASVTKCSISKLELSAEOELLTLPSLE 1080  
 QY 1081 SLEVSSTIOSQODIPFNLLKFCCLKELSDVEENINVSFVPEEPFNHMMELLIQISA 1140  
 DB 1081 SLEVSSTIOSQODIPFNLLKFCCLKELSDVEENINVSFVPEEPFNHMMELLIQISA 1140  
 QY 1141 EYDPSLTVLKIQNSPMLHVEHLKCNFFSPDGSMTLVSCCKLTKFSDSPFOAVPVA 1200  
 DB 1141 EYDPSLTVLKIQNSPMLHVEHLKCNFFSPDGSMTLVSCCKLTKFSDSPFOAVPVA 1200  
 QY 1201 SLPNFISLKIINLEGGQFPDEBTSEKFAVILGSLNLEBLLPTGDGIYVAKLLIQCCQ 1260  
 DB 1201 SLPNFISLKIINLEGGQFPDEBTSEKFAVILGSLNLEBLLPTGDGIYVAKLLIQCCQ 1260  
 QY 1261 QHLCLAVLSPFKTLNDSVVEIKVAISGGFQCLNMLKLSINKKITEEGYRNFQALDWM 1320  
 DB 1261 QHLCLAVLSPFKTLNDSVVEIKVAISGGFQCLNMLKLSINKKITEEGYRNFQALDWM 1320  
 QY 1321 PNLQELDISRHFTFCIKAAQATTVKSLSQCVLRPLRLRLNMLSWLDDADIALANWKER 1380  
 DB 1321 PNLQELDISRHFTFCIKAAQATTVKSLSQCVLRPLRLRLNMLSWLDDADIALANWKER 1380  
 QY 1381 HPOSXYLLTIQKWLFPFSPILQK 1403  
 DB 1381 HPOSXYLLTIQKWLFPFSPILQK 1403

RESULT 2  
 AA14079  
 ID AA14079 standard; Protein; 1403 AA.

XX AA14079;

DT 20-JUL-1999 (first entry)

XX Gonadotropic hormone protein sequence.

XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;

XX totipotent cell; somatic cell chromosome.

XX Homo sapiens.

XX JP11113444-A.

XX 27-APR-1999.

XX 14-OCT-1997; 97JP-0280830.

XX 14-OCT-1997; 97JP-0280830.

XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

XX (SAKA/) SAKAI H.

XX WPI: 1999-320709/27.

XX N-PSDB; AAX58000.

XX An excessive ovulation animal - useful for improving the

XX productivity of animals

XX Claim 3; Page 11-14; 18pp; Japanese.

XX This sequence represents a gonadotropic hormone.

XX The invention relates to an excessive ovulation animal, which is a

XX transgenic animal with a totipotent cell containing a DNA fragment

XX containing a promoter sequence and a gonadotropic hormone coding

XX sequence. The DNA fragment is in the somatic cell chromosome. The

XX excessive ovulation animal is useful for improving the productivity of

XX animals. The method can improve the productivity of a useful animal.

Query Match 100.0%; Score 1403; DB 20; Length 1403;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATOOKASDERISQPDHNLPELSALLGIDAVALKELEEEOKRARKQKYNQMSSE 60  
 DB 1 MATOOKASDERISQPDHNLPELSALLGIDAVALKELEEEOKRARKQKYNQMSSE 60  
 QY 61 AKRLKTFVYBYEYSYSSIPQEMAAAGFYFTGVSGIQCFCSLLFGAGLTRPIEDHKRF 120  
 DB 61 AKRLKTFVYBYEYSYSSIPQEMAAAGFYFTGVSGIQCFCSLLFGAGLTRPIEDHKRF 120  
 QY 121 HPDCEGLNKNQDGNIAKTDIRVKNLKSRLRGKMYOYSEBARLASFRNMPFYVQGISPCV 180  
 DB 121 HPDCEGLNKNQDGNIAKTDIRVKNLKSRLRGKMYOYSEBARLASFRNMPFYVQGISPCV 180  
 QY 181 LEBAGFVFPKQDITYQCSGCCGCLGNWEEGDDPKWHAAMFKCFGLSKSSSEITQYI 240  
 DB 181 LEBAGFVFPKQDITYQCSGCCGCLGNWEEGDDPKWHAAMFKCFGLSKSSSEITQYI 240  
 QY 241 QSYKGFVDITGSHFVNSWQRELPMASAYCNDSTPAYEELRLDSFKDMPRESAVGVAALA 300  
 DB 241 QSYKGFVDITGSHFVNSWQRELPMASAYCNDSTPAYEELRLDSFKDMPRESAVGVAALA 300  
 QY 301 KAGLFYTGIKDITVQCFSCGCGCLEKWOEGDDPLDHTRCFPNCFQNMKSSABVTPLDLOS 360  
 DB 301 KAGLFYTGIKDITVQCFSCGCGCLEKWOEGDDPLDHTRCFPNCFQNMKSSABVTPLDLOS 360  
 QY 361 RGEICELLETTSSENLSDSIAGPIVPEMAQCEAQMFOEAKRLNQLRAAYTSASFRRHS 420  
 DB 361 RGEICELLETTSSENLSDSIAGPIVPEMAQCEAQMFOEAKRLNQLRAAYTSASFRRHS 420  
 QY 421 LLDISSDLATDHLIGCDLSIAKHSISKVQEPVLYPEVNGNLSVMCVGEAGSGCTVLL 480  
 DB 421 LLDISSDLATDHLIGCDLSIAKHSISKVQEPVLYPEVNGNLSVMCVGEAGSGCTVLL 480  
 QY 481 KXIAPLWASGCCPLNRFQVLFVYLSLSTRPDEGLASIIDOLLEKESGVTEMCNRIIO 540  
 DB 481 KXIAPLWASGCCPLNRFQVLFVYLSLSTRPDEGLASIIDOLLEKESGVTEMCNRIIO 540  
 QY 541 QLNQOVLFLDDYKEICSIPOVITGKLIQKNHLSRTCLIAVTNRARDIRRYLETILEIK 600  
 DB 541 QLNQOVLFLDDYKEICSIPOVITGKLIQKNHLSRTCLIAVTNRARDIRRYLETILEIK 600  
 QY 601 APPFYNTVCILRLKLSHMTTRLRKFMVYFGKQNSLOKIOKTPLAATICAHPFOYPPDS 660  
 DB 601 APPFYNTVCILRLKLSHMTTRLRKFMVYFGKQNSLOKIOKTPLAATICAHPFOYPPDS 660  
 QY 661 FDDVAVFESYMERLSLRNKATAEILKATYSSCGELALNGFSCCFEFDNDDLAEGVDED 720  
 DB 661 FDDVAVFESYMERLSLRNKATAEILKATYSSCGELALNGFSCCFEFDNDDLAEGVDED 720  
 QY 721 EDUTNCLMSKFTAQRILRPYRFLSPAQFQFLAGMLIELLDSRQHQDLGJYHLKQINS 780  
 DB 721 EDUTNCLMSKFTAQRILRPYRFLSPAQFQFLAGMLIELLDSRQHQDLGJYHLKQINS 780  
 QY 781 PMMTVSAYNNFLNYSLSLPSTAGKRYVSHLHLVDNKSLENISBNDYLGHQBPISIQ 840  
 DB 781 PMMTVSAYNNFLNYSLSLPSTAGKRYVSHLHLVDNKSLENISBNDYLGHQBPISIQ 840  
 QY 841 MQLLGLMOICPOAVFMSVSEHLVLAALKTAVQSNVTVAACSPVLOFLOGRTLTGALNL 900  
 DB 841 MQLLGLMOICPOAVFMSVSEHLVLAALKTAVQSNVTVAACSPVLOFLOGRTLTGALNL 900  
 QY 901 QYFDPHPSLSLRSIHPIRINKTSPPRAHFSVLETCDDKQSVPTIDQYASAFPMNMW 960  
 DB 901 QYFDPHPSLSLRSIHPIRINKTSPPRAHFSVLETCDDKQSVPTIDQYASAFPMNMW 960  
 QY 961 EBNLAKEKNVNSYNDMQRASPDISTGYWKLSPPQYKICPLEVYNDIDVVGQDMLLETL 1020  
 DB 961 EBNLAKEKNVNSYNDMQRASPDISTGYWKLSPPQYKICPLEVYNDIDVVGQDMLLETL 1020  
 QY 1021 MTFVFSASQRIEHLNHSRGFISIRPALELSKASVTKCSISKLELSAEOELLTLPSLE 1080

```

Db 1021 MTFVSAQRLELHNSRGFIESIRPALBLSKASVTKCSISKLELSAAEOELTLTLPSELE 1080
QY 1081 SLEVSCTIGSQODQIFPMLDKFLCKELSVDEGNINVSFVIDEFPFNHMEKLLIOISA 1140
Db 1081 SLEVSCTIGSQODQIFPMLDKFLCKELSVDEGNINVSFVIDEFPFNHMEKLLIOISA 1140
QY 1141 EYDPSKLVKLIQNSPMLHVFHLKCNFSDPSGLMTMLVSCCKLTETKSDSFQAVPFA 1200
Db 1141 EYDPSKLVKLIQNSPMLHVFHLKCNFSDPSGLMTMLVSCCKLTETKSDSFQAVPFA 1200
QY 1201 SLNPFSLKILNLEGGQFPDEBTSEKFAVILGSLNMBELILPTGDDGIYRAKLLIQCCQ 1260
Db 1201 SLNPFSLKILNLEGGQFPDEBTSEKFAVILGSLNMBELILPTGDDGIYRAKLLIQCCQ 1260
QY 1261 QHCLRLVLSFFKTLNDDSVVEIAKVAISGFOKLENKLSINHKTIEGYRNFPOALDMN 1320
Db 1261 QHCLRLVLSFFKTLNDDSVVEIAKVAISGFOKLENKLSINHKTIEGYRNFPOALDMN 1320
QY 1321 PMLQBLDISRHFTETCIKAQATTVKSLSQCVLRLPRLIRLNLMSWLDADADIALNWKER 1380
Db 1321 PMLQBLDISRHFTETCIKAQATTVKSLSQCVLRLPRLIRLNLMSWLDADADIALNWKER 1380
QY 1381 HPOSRYTLTIQKMLLPSPPIQK 1403
Db 1381 HPOSRYTLTIQKMLLPSPPIQK 1403

```

## RESULT 3

AA09539

ID AA09539 standard; Protein: 1403 AA.

AC AA09539;

DT 20-JUL-1999 (first entry)

DE Human apoptosis inhibiting protein #1.

KM Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;

OS Homo sapiens.

PN JP1116599-A.

PD 27-APR-1999.

PF 14-OCT-1997; 97JP-0280831.

PR 14-OCT-1997; 97JP-0280831.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR MPI: 1999-323531/27.

N-PSDB; AAX56272.

PT New apoptosis inhibitory protein - useful for determining mechanism

CC of various apoptotic diseases e.g. human spinal muscular atrophy

CC The present sequence represents a human apoptosis inhibitory protein.

CC The mechanism of various apoptotic diseases such as human spinal

CC muscular atrophy and the diagnosis, the prevention and the treatment

CC of such diseases.

SQ Sequence 1403 AA;

Query Match 100.0%; Score 1403; DB 20; Length 1403;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MATQKASDERISQFDHNLPELSALLGLDAVOLAKELFEEOKEKAKQKYNQMRSE 60
Db 1 MATQKASDERISQFDHNLPELSALLGLDAVOLAKELFEEOKEKAKQKYNQMRSE 60
QY 61 AKRLKFTVTPYSSSWIPEMAAAGPYFTGVKSGIQCFCCSLTFSGAGLTRLPIEDHKRF 120
Db 61 AKRLKFTVTPYSSSWIPEMAAAGPYFTGVKSGIQCFCCSLTFSGAGLTRLPIEDHKRF 120
QY 121 HPDCGFLNKDVGNIAKYDRIYKLNKSLRPLGCKMRQVEBARLASFRNMPFYQGISPCV 180
Db 121 HPDCGFLNKDVGNIAKYDRIYKLNKSLRPLGCKMRQVEBARLASFRNMPFYQGISPCV 180
QY 181 LSEAGFVFTKODTVQCFSCGCGCLGNMBEGDDPMKEHAKMFKCEFLSKXSSEETIYI 240
Db 181 LSEAGFVFTKODTVQCFSCGCGCLGNMBEGDDPMKEHAKMFKCEFLSKXSSEETIYI 240
QY 241 QSYKGFVDITGEHFVNSWQRELPMAASACNDSIYAYEELRLDSFKDMPRESAVGVALA 300
Db 241 QSYKGFVDITGEHFVNSWQRELPMAASACNDSIYAYEELRLDSFKDMPRESAVGVALA 300
QY 301 KAGLFYTGIKDIYQCFSCGCGCLEKQEGDDPLDHTTRCFPNCPPFLQWKSABVTPLDS 360
Db 301 KAGLFYTGIKDIYQCFSCGCGCLEKQEGDDPLDHTTRCFPNCPPFLQWKSABVTPLDS 360
QY 361 RGELECELTETSESNLSDSIAGPIVPEMAQGEAQMVEAKNLNEQLRAAYTSAPRHS 420
Db 361 RGELECELTETSESNLSDSIAGPIVPEMAQGEAQMVEAKNLNEQLRAAYTSAPRHS 420
QY 421 LDISSDATDHLACCDLSIASKHISKRVQEPVLPEVFNLSVWKEGASGGTYVL 480
Db 421 LDISSDATDHLACCDLSIASKHISKRVQEPVLPEVFNLSVWKEGASGGTYVL 480
QY 481 KXIAFLMASGCCPLNRFQVFLYLSSTRPDGLASITCDOLLEEGSVTECMKNIIQ 540
Db 481 KXIAFLMASGCCPLNRFQVFLYLSSTRPDGLASITCDOLLEEGSVTECMKNIIQ 540
QY 541 QLKQOVLFLDDYKEISIPQVIGKLIQKNLSRTCLLAVTNRARDIRRYLETLEIK 600
Db 541 QLKQOVLFLDDYKEISIPQVIGKLIQKNLSRTCLLAVTNRARDIRRYLETLEIK 600
QY 601 AFPPYNTVCILRKLFSHNMTLRKPMVYFGKQNSLOKIOKTLFVAALCAHMFQYFPDS 660
Db 601 AFPPYNTVCILRKLFSHNMTLRKPMVYFGKQNSLOKIOKTLFVAALCAHMFQYFPDS 660
QY 661 FDDVAVFKSYMERLSLNKATAEILKATVSSCGELAKGFFSCCFEPDDDLAEGVDED 720
Db 661 FDDVAVFKSYMERLSLNKATAEILKATVSSCGELAKGFFSCCFEPDDDLAEGVDED 720
QY 721 EDLTWCLMSKFTAQRLRPYRFISPAFOEFLAGMLIELLSDQEOHODLGLYHLKQINS 780
Db 721 EDLTWCLMSKFTAQRLRPYRFISPAFOEFLAGMLIELLSDQEOHODLGLYHLKQINS 780
QY 781 PMMTVASNNPFLNYSLSLPTAGPKIVSHLHLVDNKESELENISENDVLYAKOPELSIQ 840
Db 781 PMMTVASNNPFLNYSLSLPTAGPKIVSHLHLVDNKESELENISENDVLYAKOPELSIQ 840
QY 841 MOLRLGLMQICPOAFSWSVSEHLVLAIKTAYOSNTVAASPFVLOPLQGRITTLGALNL 900
Db 841 MOLRLGLMQICPOAFSWSVSEHLVLAIKTAYOSNTVAASPFVLOPLQGRITTLGALNL 900
QY 901 OYFDPHPSLSILASIHPIRGNTSPRAHFSVLETCFDSQVPTIDQVYASAFBPMNM 960
Db 901 OYFDPHPSLSILASIHPIRGNTSPRAHFSVLETCFDSQVPTIDQVYASAFBPMNM 960
QY 961 ERNLAEKEDNVKSYMDQORASPDLSGTGYKLSPKQYKPCLEVDVNDIDVVGOMLETL 1020
Db 961 ERNLAEKEDNVKSYMDQORASPDLSGTGYKLSPKQYKPCLEVDVNDIDVVGOMLETL 1020
QY 1021 MTFVSAQRLELHNSRGFIESIRPALBLSKASVTKCSISKLELSAAEOELTLTLPSELE 1080
Db 1021 MTFVSAQRLELHNSRGFIESIRPALBLSKASVTKCSISKLELSAAEOELTLTLPSELE 1080
QY 1081 SLEVSCTIGSQODQIFPMLDKFLCKELSVDEGNINVSFVIDEFPFNHMEKLLIOISA 1140

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Db      1081 SLEVSQITQSOQOIPNIDKFLCLKELSYDLEGNINVSVPDEEPNPFHMEKLIQISA 1140
Qy      1141 EYDPSKLVKLIONSNLHVFHLKCNFPSPDPSGLMTLVSCCKLTETIKSDSPFOAVPFA 1200
Db      1141 EYDPSKLVKLIONSNLHVFHLKCNFPSPDPSGLMTLVSCCKLTETIKSDSPFOAVPFA 1200
Qy      1201 SLNPNISLKIINLESCQFPDEETSEKFAIIGLSNLBELIPTDGIYRVAKLIIOCCQ 1260
Db      1201 SLNPNISLKIINLESCQFPDEETSEKFAIIGLSNLBELIPTDGIYRVAKLIIOCCQ 1260
Qy      1261 QHCLRLVTSFPEKTLNDDSVVEIAKVAISGGFQKLENLKLISNHKITEGYNFQALDNM 1320
Db      1261 QHCLRLVTSFPEKTLNDDSVVEIAKVAISGGFQKLENLKLISNHKITEGYNFQALDNM 1320
Qy      1321 PNLQELDISRHTECKIKQATVKSLSQCVLRLPRLIRLNMLSMLDDADILLVNMR 1380
Db      1321 PNLQELDISRHTECKIKQATVKSLSQCVLRLPRLIRLNMLSMLDDADILLVNMR 1380
Qy      1381 HPOSKYTLTLOKMLPFSPIIOK 1403
Db      1381 HPOSKYTLTLOKMLPFSPIIOK 1403

```

RESULT 4  
AA588053  
ID AA588053 standard; Protein; 1403 AA.

AA588053;

22-SEP-2000 (first entry)

Human NAIP protein.

NAIP; apoptosis inhibiting protein; monoclonal antibody; diagnosis; apoptosis disease onset mechanism; drugs development; prevention; treatment; human.

Homo sapiens.

Key Location/Qualifiers  
Region 256..586  
/note= "Immunogenic region, specifically described in Claim 1"  
Region 841..1052  
/note= "Immunogenic region, specifically described in Claim 1"

WO200024889-A1.

04-MAY-2000.

22-OCT-1999; 99WO-JP05841.

26-OCT-1998; 98JP-0304550.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

(SAKAI/) SAKAI H.

Sakai H, Ikeda J;

WPI; 2000-350731/30.

N-PsDB; AAA39808.

Simple and accurate quantitation of human apoptosis inhibitory protein (NAIP) with monoclonal antibodies, for disease diagnosis and development of drugs to prevent and treat apoptosis-related diseases

Claim 1; Page 24-30; 36pp; Japanese.

This invention describes novel anti-NAIP monoclonal antibodies, produced by hybridomas, prepared by fusing antibody-producing cells of mammals immunized with an immunogen containing residues 256-586 or 841-1052 of a

CC 1403 residue amino acid sequence, fully defined in the specification, or  
CC their partial sequence, with a myeloma cell line. The monoclonal  
CC antibodies are for the study of apoptosis disease onset mechanism,  
CC disease diagnosis and development of drugs to prevent and treat  
CC apoptosis-related diseases. The quantitation method with the monoclonal  
CC antibodies is simple and accurate by using a biological specimen. This  
CC sequence represents the human apoptosis inhibitory protein NAIP which is  
CC described in the method of the invention.

Sequence 1403 AA:

Query Match 100.0%; Score 1403; DB 21; Length 1403;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MATQKASDERISQPDHNLPELSALGLDAVOLAKHEEBOEKERAKQKYSQMRSE 60
Db      1 MATQKASDERISQPDHNLPELSALGLDAVOLAKHEEBOEKERAKQKYSQMRSE 60
Qy      61 AKRLKTFVTEPYSSWIPQENAAAGFTYGVKSGIQCCSLIFGAGLTRLPIDHRKF 120
Db      61 AKRLKTFVTEPYSSWIPQENAAAGFTYGVKSGIQCCSLIFGAGLTRLPIDHRKF 120
Qy      121 HPDCGFLNKQVGNIAKYDIRVKQLKSRLRGCKMRKYOEERLASFRNWPPYVQGISPCV 180
Db      121 HPDCGFLNKQVGNIAKYDIRVKQLKSRLRGCKMRKYOEERLASFRNWPPYVQGISPCV 180
Qy      181 LSEAGFVETGKODTVQCCSCGCGCAGNMEEGDDPMKEHAKMFKCFELASKSSSEITQYI 240
Db      181 LSEAGFVETGKODTVQCCSCGCGCAGNMEEGDDPMKEHAKMFKCFELASKSSSEITQYI 240
Qy      241 OSYKGFVDITGSHFVNSVQRELPMASAYCNDSTIFAYEELRLDSFKDMPRESAVGAAIA 300
Db      241 OSYKGFVDITGSHFVNSVQRELPMASAYCNDSTIFAYEELRLDSFKDMPRESAVGAAIA 300
Qy      301 KAGLFYTGIDKIIVQCFSCGCGCLEKQEGDDPLDHTRCFPCNCFLONNKSSAEVTPDIQS 360
Db      301 KAGLFYTGIDKIIVQCFSCGCGCLEKQEGDDPLDHTRCFPCNCFLONNKSSAEVTPDIQS 360
Qy      361 RGEICELLETTSESNSLEISIAVGPVPEMAQGEAMFQENAKNLEQLAAATYSAPFRMS 420
Db      361 RGEICELLETTSESNSLEISIAVGPVPEMAQGEAMFQENAKNLEQLAAATYSAPFRMS 420
Qy      421 LLDISSDLATPHLACDLSIASKHISKVPQEBLVPEVFGNLSNVCYEGEAGSCKTYLL 480
Db      421 LLDISSDLATPHLACDLSIASKHISKVPQEBLVPEVFGNLSNVCYEGEAGSCKTYLL 480
Qy      481 KKIATFLMAGCCPILNRQVLVYLSLSTRPDEGLASIIICDULEKESVTEMCKRNTIQ 540
Db      481 KKIATFLMAGCCPILNRQVLVYLSLSTRPDEGLASIIICDULEKESVTEMCKRNTIQ 540
Qy      541 QLNQOVLFLDDYKEICISIPQYIGLIDQNLSTRCLLIIVRTNARDIRRLETLLEIK 600
Db      541 QLNQOVLFLDDYKEICISIPQYIGLIDQNLSTRCLLIIVRTNARDIRRLETLLEIK 600
Qy      601 AFPPYNTVCILRKLFSSHMTLRKRMVYFGKQOSIQKIQKPLFVAALCAHMFQPPDS 660
Db      601 AFPPYNTVCILRKLFSSHMTLRKRMVYFGKQOSIQKIQKPLFVAALCAHMFQPPDS 660
Qy      661 FDDVAVFYSYMERLSLRNKATABIILKATVSSGCEIALGPFSCCFEPDDDLAEGVDB 720
Db      661 FDDVAVFYSYMERLSLRNKATABIILKATVSSGCEIALGPFSCCFEPDDDLAEGVDB 720
Qy      721 EDLTKMSKPTAQCRLRPYRFLSAFOEPLAGRLIELSDROREHDDGILYHKQINS 780
Db      721 EDLTKMSKPTAQCRLRPYRFLSAFOEPLAGRLIELSDROREHDDGILYHKQINS 780
Qy      781 PMMTVSAYNNFLNYYSSLPSTKAGPKIVSHLLHVDNKESENISENDYLGKQPSIQ 840
Db      781 PMMTVSAYNNFLNYYSSLPSTKAGPKIVSHLLHVDNKESENISENDYLGKQPSIQ 840
Qy      841 MQLRLGLQICEQAVFSNVSEHLVLAALKTAVQSNVAAAGPVLQILOGRTLTIGALNT 900
Db      841 MQLRLGLQICEQAVFSNVSEHLVLAALKTAVQSNVAAAGPVLQILOGRTLTIGALNT 900

```

Db	841	MQLRLGLMQLCPQAVYFSKNVSEHLLVLAKTAYQSGNTVAACSPFVLQFLQGRITLTIGALNTL	900
Qy	901	QYFPDHPESLSLNSIHFPRIKNGTSPRAHPSVLETGCDKSGVPTIDODYASAPERNEN	960
Db	901	QYFPDHPESLSLNSIHFPRIKNGTSPRAHPSVLETGCDKSGVPTIDODYASAPERNEN	960
Qy	961	ERNLAEEKEDNVKSYMDQORRASPDLSTGYWKLSPKQYKICPLEVDVNDIDVGDMLLEIT	102
Db	961	ERNLAEEKEDNVKSYMDQORRASPDLSTGYWKLSPKQYKICPLEVDVNDIDVGDMLLEIT	102
Qy	1021	MTVFSASQRIEHLNHSRGFTESIRPALTELSTKASYTKCSISKTELSAAEGELLTLPSLE	108
Db	1021	MTVFSASQRIEHLNHSRGFTESIRPALTELSTKASYTKCSISKTELSAAEGELLTLPSLE	108
Qy	1081	SLVSGTIGSQDQDIPFLNDKFLCLKEISVDLEGNINVFSAVPEEPNPFHMEKLTIGISA	114
Db	1081	SLVSGTIGSQDQDIPFLNDKFLCLKEISVDLEGNINVFSAVPEEPNPFHMEKLTIGISA	114
Qy	1141	EYDPSKLVKIKIONSPMLHVFHLKCNFPDSDGSLMTLVGCKKLTETKESDSFFQAVPVA	120
Db	1141	EYDPSKLVKIKIONSPMLHVFHLKCNFPDSDGSLMTLVGCKKLTETKESDSFFQAVPVA	120
Qy	1201	SLPNFISLKLINLEGOQFPDEETSEKFAVILGSLNLEBILPTGDIYRAVKLTIIQOCQ	126
Db	1201	SLPNFISLKLINLEGOQFPDEETSEKFAVILGSLNLEBILPTGDIYRAVKLTIIQOCQ	126
Qy	1261	QLHCLRVLSPEKTLNDSVVEIAKVAISGCFQKLEMLKLSINHKTTEEGYRNFQALDNM	132
Db	1261	QLHCLRVLSPEKTLNDSVVEIAKVAISGCFQKLEMLKLSINHKTTEEGYRNFQALDNM	132
Qy	1321	PNLQELDISRHFTETCICAQATTWKSLSQCVLRPLIRLNLMSWLLDDADIALNVMKER	138
Db	1321	PNLQELDISRHFTETCICAQATTWKSLSQCVLRPLIRLNLMSWLLDDADIALNVMKER	138
Qy	1381	HQSKYLTTLQKWLIPSPPIQK 1403	
Db	1381	HQSKYLTTLQKWLIPSPPIQK 1403	
RESULT 5			
ABP72166			
ID	ABP72166	standard, protein, 1403 AA.	
XX	ABP72166;		
AC	ABP72166;		
DT	22-APR-2003	(first entry)	
XX			
DE		Human inhibitor of apoptosis protein NIP.	
XX			
KW		Inhibitor of apoptosis; NIP, human; apoptosis; cancer; leukaemia;	
KW		lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic;	
XX		gene therapy.	
OS		Homo sapiens.	
XX			
PN	MO2003004606-A2.		
XX			
PD	16-JUN-2003.		
XX			
PP	03-JUL-2002; 2002MO-US21002.		
XX			
PR	03-JUL-2001; 2001US-0898158.		
XX			
PA	(UYCO ) UNIV COLUMBIA NEW YORK.		
XX			
PI	Troy CM, Shelanski ML;		
XX			
DR	WPI; 2003-210351/20.		
XX			
PT	New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for		
XX	treating cancer, neurodegenerative disorder or cardiomyopathy -		
XX	Disclosure; Fig 24A-C; 124bp; Ecol118b.		
XX			

XX The present sequence is the protein sequence of human inhibitor of  
CC apoptosis protein XIAP. The invention provides a nucleic acid,  
CC such as an antisense oligonucleotide, which specifically hybridises  
CC to a nucleic acid encoding an inhibitor of apoptosis protein,  
CC especially MIAP1, MIAP2, MIAP3, CIAP1, CIAP2 and XIAP. A claimed  
CC method for inducing a cell's death comprises contacting the cell  
CC with the nucleic acid under conditions permitting the nucleic acid  
CC to enter the cell, especially the use of a vector, liposome, or a  
CC mechanical or electrical means. The method is used to treat acute  
CC lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer,  
CC breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's  
CC disease, malignant melanoma, neuroblastoma, renal cell carcinoma  
CC and squamous cell carcinoma (all claimed).

Query Match	100.0%	Score 1403	DB 24	Length 1403
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1403	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MATQKASDERISQFPHNLPELSALLIGDAVQALKELEEEQKRAKQKYNQMRSE	60	
DB	1	MATQKASDERISQFPHNLPELSALLIGDAVQALKELEEEQKRAKQKYNQMRSE	60	
QY	61	AKRLKFTVTEPYSSWIPOEMAAGFYFTGVNSGICQCCSLLIFGAGITRLPIEDHGRF	120	
DB	61	AKRLKFTVTEPYSSWIPOEMAAGFYFTGVNSGICQCCSLLIFGAGITRLPIEDHGRF	120	
QY	121	HPDCCGLMKDVGNIATKDIRYKNIKSLRGKGRKYQEBEARPLASFRNMPFYVGISPCV	180	
DB	121	HPDCCGLMKDVGNIATKDIRYKNIKSLRGKGRKYQEBEARPLASFRNMPFYVGISPCV	180	
QY	181	LSBAGFVPTGKODTVQCFSCGCGCLGNREEGDDPMWEHAKMPKPKCEPLRSKSSSEITQYI	240	
DB	181	LSBAGFVPTGKODTVQCFSCGCGCLGNREEGDDPMWEHAKMPKPKCEPLRSKSSSEITQYI	240	
QY	241	QSYKGFVDITGHHFVNSVQRELPMASAYCNDISIYAYEBRLDPSFKDMPRESAGVAAAL	300	
DB	241	QSYKGFVDITGHHFVNSVQRELPMASAYCNDISIYAYEBRLDPSFKDMPRESAGVAAAL	300	
QY	301	KGLPYTGTGKIOVQCFSCGCGCLGNREEGDDDLDDHTCSPKPCPLQNMKSSAEVTPDLOS	360	
DB	301	KGLPYTGTGKIOVQCFSCGCGCLGNREEGDDDLDDHTCSPKPCPLQNMKSSAEVTPDLOS	360	
QY	361	RGEICELLETTSESNLEDSIIVGPIVEBMAQGEAQMFOQAKNLINBQURLAAYTSAPRHS	420	
DB	361	RGEICELLETTSESNLEDSIIVGPIVEBMAQGEAQMFOQAKNLINBQURLAAYTSAPRHS	420	
QY	421	LLDISSDLATLHLGCSLSTASKRISRPVQEPVLPREVGNLNSVMCVEGEAGSGKTVLL	480	
DB	421	LLDISSDLATLHLGCSLSTASKRISRPVQEPVLPREVGNLNSVMCVEGEAGSGKTVLL	480	
QY	481	KKIAFLMASGCCPLNRFQVLYFVYLSASTSPDGLASITCDOLLEKGSYTEMCMNIIQ	540	
DB	481	KKIAFLMASGCCPLNRFQVLYFVYLSASTSPDGLASITCDOLLEKGSYTEMCMNIIQ	540	
QY	541	QKKNQVPLLDYKEICISIPQYIGKLIQKNHSRTCLLAVRTNRRARDIRRYLETILEIK	600	
DB	541	QKKNQVPLLDYKEICISIPQYIGKLIQKNHSRTCLLAVRTNRRARDIRRYLETILEIK	600	
QY	601	AFPPYNNVCLRLKFSNNMTRLRKFMVYFGKQISLOKIQKTPLFVAALCAHFOYFPDPS	660	
DB	601	AFPPYNNVCLRLKFSNNMTRLRKFMVYFGKQISLOKIQKTPLFVAALCAHFOYFPDPS	660	
QY	661	FDDVAVFKSIMERLSLRNKATAEILKATYSSCGEALIKGPFSCCFEPNDDILAEAGVDED	720	
DB	661	FDDVAVFKSIMERLSLRNKATAEILKATYSSCGEALIKGPFSCCFEPNDDILAEAGVDED	720	
QY	721	EDUTMCLMSKFTNQRRLPFRPLSPAFOEFLAGMRLIELLDSROBHDQILYHLKQINS	780	
DB	721	EDUTMCLMSKFTNQRRLPFRFRPLSPAFOEFLAGMRLIELLDSROBHDQILYHLKQINS	780	

```

OY 781 PMMTVSAYNNFLNYSSLPSTYKAGPKIVSHLLHLVDNKNSELENISENDYLGKQPEISIQ 840
DB 781 PMMTVSAYNNFLNYSSLPSTYKAGPKIVSHLLHLVDNKNSELENISENDYLGKQPEISIQ 840
OY 841 MOLARGIMQICQOAFPSWVSEHLVLTAKTAYOSMTVAACSPVLOFQGRITLTGANTL 900
DB 841 MOLARGIMQICQOAFPSWVSEHLVLTAKTAYOSMTVAACSPVLOFQGRITLTGANTL 900
OY 901 QYFDPHPSLSLRISIRHPFIRGNKTSPPRAHFSVLETCFPGKSQVPTTIDODYASAFEPNEM 960
DB 901 QYFDPHPSLSLRISIRHPFIRGNKTSPPRAHFSVLETCFPGKSQVPTTIDODYASAFEPNEM 960
OY 961 EBNLAKEKDNVKSVMQORRASPDLSTGYWKLSPQYKIPCLIEVDVNDIDVVGQDMLEIL 1020
DB 961 EBNLAKEKDNVKSVMQORRASPDLSTGYWKLSPQYKIPCLIEVDVNDIDVVGQDMLEIL 1020
OY 1021 MTFVFSASQRIEHLNHSRGFISIRPALELSQAATYTKSISKLELSAAEQELMLTLPSE 1080
DB 1021 MTFVFSASQRIEHLNHSRGFISIRPALELSQAATYTKSISKLELSAAEQELMLTLPSE 1080
OY 1081 SLEVSGTIOQODQIFPNLDKFLCLKELSVLEGNINVSFVPEEPFNPHMEKLIHQISA 1140
DB 1081 SLEVSGTIOQODQIFPNLDKFLCLKELSVLEGNINVSFVPEEPFNPHMEKLIHQISA 1140
OY 1141 EYDPSKLVLTIONSPNLHVFLKCNFSPDFGSLMTMLVSCKLTEIKESDSFFQAVPEVA 1200
DB 1141 EYDPSKLVLTIONSPNLHVFLKCNFSPDFGSLMTMLVSCKLTEIKESDSFFQAVPEVA 1200
OY 1201 SLNPFISLKLINLECOQFPDEETSEKFAVILGSLNLEELIIPITGDIYRVAKLIIQOQ 1260
DB 1201 SLNPFISLKLINLECOQFPDEETSEKFAVILGSLNLEELIIPITGDIYRVAKLIIQOQ 1260
OY 1261 QHCHGRVLSFFKTLNDDSVVEIAKVAISGGFQKLEMLKISINHKTTEEGYRNPFOALNM 1320
DB 1261 QHCHGRVLSFFKTLNDDSVVEIAKVAISGGFQKLEMLKISINHKTTEEGYRNPFOALNM 1320
OY 1321 PNLQELDISRHFTTECIKAQATTVKSLSQCVLRPLRILRLMLSWLDDADIALNLVWKER 1380
DB 1321 PNLQELDISRHFTTECIKAQATTVKSLSQCVLRPLRILRLMLSWLDDADIALNLVWKER 1380
OY 1381 HPQSKYLTLLQWMLPFPPIIOK 1403
DB 1381 HPQSKYLTLLQWMLPFPPIIOK 1403
OY 1381 HPQSKYLTLLQWMLPFPPIIOK 1403
DB 1381 HPQSKYLTLLQWMLPFPPIIOK 1403

```

## RESULT 6

ABU07400 standard; Protein; 1403 AA.

AC ABU07400;

DT 28-JAN-2003 (first entry)

DE Protein differentially regulated in prostate cancer #3.

KM Prostate cancer; gene expression; differential regulation;  
 KM molecular marker; drug target; cancer detection; cancer diagnosis;  
 KM cancer staging; cancer grading; cancer assessing; cancer monitoring.

OS Homo sapiens.

PN MO200281638-AA2.

PD 17-OCT-2002.

PF 08-APR-2002; 2002W0-US10824.

PR 06-APR-2001; 2001US-281731P.

PA (ORIG-) ORIGENE TECHNOLOGIES INC.

PI Sun Z, Jay G;

```

XX WPI; 2003-058520/05.
DR
XX
PT Novel genes which are differentially regulated in prostate cancer,
PT useful for diagnosing prostate cancer in prostate tissue sample and
PT assessing therapeutic or preventive intervention in prostate cancer
PT patients.
PS
XX Claim 1; Page 202-206; 416pp; English.
XX
CC The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity.
CC (I) is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is
CC useful in therapeutic applications to treat prostate cancer. The
CC identification of specific genes, and groups of genes, expressed in
CC pathways physiologically relevant to prostate cancer permits the
CC definition of functional and disease pathways and the delineation of
CC targets in these pathways which are useful in diagnostic, therapeutic,
CC and clinical applications. This is the amino acid sequence of a protein
CC differentially regulated in prostate cancer.
XX
SQ Sequence 1403 AA:
Query Match 100.0%; Score 1403; DB 24; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MATQOKASDERISQPDNHLPELSALLGLDAVOLAKLEBEBQKRAKQKYNQMSR 60
DB 1 MATQOKASDERISQPDNHLPELSALLGLDAVOLAKLEBEBQKRAKQKYNQMSR 60
OY 61 AKRLTPTVYBYSWIMQEMAAAGFYTGYSIGQCCSILTGAGLTRLPIDHRRF 120
DB 61 AKRLTPTVYBYSWIMQEMAAAGFYTGYSIGQCCSILTGAGLTRLPIDHRRF 120
OY 121 HPDCGFLANKQVGNIAKTDIRVKNLSRLRGKMRVQSEEARLASFRWMPFYVQGISPCV 180
DB 121 HPDCGFLANKQVGNIAKTDIRVKNLSRLRGKMRVQSEEARLASFRWMPFYVQGISPCV 180
OY 181 LSEAGFVFTGKODTYQCSGCGCLNWEBGDDPMKEHAKWPKCFPLASKSSBEITQYI 240
DB 181 LSEAGFVFTGKODTYQCSGCGCLNWEBGDDPMKEHAKWPKCFPLASKSSBEITQYI 240
OY 241 OSYKGFVDITGEHFNYSWVQRELPMASAYCNDISIFAYSELRLDSFKDMPRESAAGVAAALA 300
DB 241 OSYKGFVDITGEHFNYSWVQRELPMASAYCNDISIFAYSELRLDSFKDMPRESAAGVAAALA 300
OY 301 KAGLFYTGIKDVIQCFSGCGCLKMQEGDDPLDHTTRCFPNCPFLONKSSAETVPDLOS 360
DB 301 KAGLFYTGIKDVIQCFSGCGCLKMQEGDDPLDHTTRCFPNCPFLONKSSAETVPDLOS 360

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Db 301 KAGLFYTGIDIVQCFSCGCGCLEKMOEGDDPLDHTTRCPNCPFLQNMKSSAETVDPLOS 360  
 QY 361 RGEICELLETSESNEEDSIAVGPVPEMAOGEAWEPEANLNEOLRAATYSAPRHS 420  
 Db 361 RGEICELLETSESNEEDSIAVGPVPEMAOGEAWEPEANLNEOLRAATYSAPRHS 420  
 QY 421 LLDISGDLATDHLJCGDUSIASKHSKPEVQEPVLPEVFGNLNSVMCEBAGSGKTVL 480  
 Db 421 LLDISGDLATDHLJCGDUSIASKHSKPEVQEPVLPEVFGNLNSVMCEBAGSGKTVL 480  
 QY 481 KKIAPLWASGCCPFLNRFQVLYSLSTRDEGLAIIICDULEKESVTEMCMNIIQ 540  
 Db 481 KKIAPLWASGCCPFLNRFQVLYSLSTRDEGLAIIICDULEKESVTEMCMNIIQ 540  
 QY 541 QLKNOVFLDDYKEICSIPOVIGKLIQKHLSTCLIAVTRNARDIRRYLETILEIK 600  
 Db 541 QLKNOVFLDDYKEICSIPOVIGKLIQKHLSTCLIAVTRNARDIRRYLETILEIK 600  
 QY 601 AAPPNTVCILRKLSHNMTLRKEMVYFGKNSLOKIQTPLEVAALCAHMFQYPPDS 660  
 Db 601 AAPPNTVCILRKLSHNMTLRKEMVYFGKNSLOKIQTPLEVAALCAHMFQYPPDS 660  
 QY 661 FDDVAVFKSYMERLSLNKATATILKATVSSCGELAKGPFSCCEPFNDODIAEGVDE 720  
 Db 661 FDDVAVFKSYMERLSLNKATATILKATVSSCGELAKGPFSCCEPFNDODIAEGVDE 720  
 QY 721 EDLTMCLMSKFTQRLRPFRPLSPAOFELAGMRLIELDSDROEHODGLYHLKQINS 780  
 Db 721 EDLTMCLMSKFTQRLRPFRPLSPAOFELAGMRLIELDSDROEHODGLYHLKQINS 780  
 QY 781 PMMTVSAVNNFLNVYSSLPSTAGPKIVSHLLHLVDNKSLENISENDYLNKHPETSLQ 840  
 Db 781 PMMTVSAVNNFLNVYSSLPSTAGPKIVSHLLHLVDNKSLENISENDYLNKHPETSLQ 840  
 QY 841 MOLLRGLMOICPOAYSVSWSEHLVLAALKTAVQSTVAAACSPVLOFLOGTTLTGALNL 900  
 Db 841 MOLLRGLMOICPOAYSVSWSEHLVLAALKTAVQSTVAAACSPVLOFLOGTTLTGALNL 900  
 QY 901 QYFPHPELSLIRSIHPPIRGNKTSPPAHFSVLETCDFKQOVPTIODYVASEPNNEM 960  
 Db 901 QYFPHPELSLIRSIHPPIRGNKTSPPAHFSVLETCDFKQOVPTIODYVASEPNNEM 960  
 QY 961 EBNLAEKEDNVASYNDMORBRASPDISTGYWLSPKQYKIPCLEVDVANDIVGQDMLELI 1020  
 Db 961 EBNLAEKEDNVASYNDMORBRASPDISTGYWLSPKQYKIPCLEVDVANDIVGQDMLELI 1020  
 QY 1021 MTFVSAQRIELHLNHSRGFIESIRPALELSKASVTCKSISKLESAABELLTLPSLE 1080  
 Db 1021 MTFVSAQRIELHLNHSRGFIESIRPALELSKASVTCKSISKLESAABELLTLPSLE 1080  
 QY 1081 SLEVGCTIQSODOI PPNLDKFLCKELSVLEGNINVSVPBEPFNHMEKLLIQISA 1140  
 Db 1081 SLEVGCTIQSODOI PPNLDKFLCKELSVLEGNINVSVPBEPFNHMEKLLIQISA 1140  
 QY 1141 EYDPSKLVKLIQNSPNLHVFLKCNFSDGSLMTMLVSCKLTETIKESDSFOAVPFA 1200  
 Db 1141 EYDPSKLVKLIQNSPNLHVFLKCNFSDGSLMTMLVSCKLTETIKESDSFOAVPFA 1200  
 QY 1201 SLRPFISLKLINLEGOFPDEETSEKRAYILGSLNLEBLLPTGNGIYRVAKLIIQCCQ 1260  
 Db 1201 SLRPFISLKLINLEGOFPDEETSEKRAYILGSLNLEBLLPTGNGIYRVAKLIIQCCQ 1260  
 QY 1261 QHLCRLVSPFKTLNDSVVEIAKVAISGGFQKLEMLKLSINHKTTEEGYRNFQALDNM 1320  
 Db 1261 QHLCRLVSPFKTLNDSVVEIAKVAISGGFQKLEMLKLSINHKTTEEGYRNFQALDNM 1320  
 QY 1321 PNLQELDISHPTECKAQAATYKSLSCVLRPLIRLNLMSWLDLADDTALNLWKKR 1380  
 Db 1321 PNLQELDISHPTECKAQAATYKSLSCVLRPLIRLNLMSWLDLADDTALNLWKKR 1380  
 QY 1381 HPQSKTLLIQKWLIPFSP110K 1403  
 Db 1381 HPQSKTLLIQKWLIPFSP110K 1403

RESULT 7  
 ID AA14080 standard; Protein, 1295 AA.  
 AC AA14080;  
 DT 20-JUL-1999 (first entry)  
 DE Gonadotropic hormone protein sequence.  
 KW Gonadotropic hormone; excessive ovulation animal; transgenic animal;  
 KW totipotent cell; somatic cell chromosome.  
 OS Homo sapiens.  
 PN JPI113444-A.  
 PD 27-APR-1999.  
 PE 14-OCT-1997; 97JP-0280830.  
 PR 14-OCT-1997; 97JP-0280830.  
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGODAN.  
 PA (SAGA/) SAKAI H.  
 DR WPI; 1999-320709/27.  
 DR N-PSDB; AAX58001.  
 PT An excessive ovulation animal - useful for improving the  
 PT productivity of animals  
 PS Claim 3; Page 14-18; 18pp; Japanese.  
 CC This sequence represents a gonadotropic hormone.  
 CC The invention relates to an excessive ovulation animal, which is a  
 CC transgenic animal with a totipotent cell containing a DNA fragment  
 CC containing a promoter sequence and a gonadotropic hormone coding  
 CC sequence. The DNA fragment is in the somatic cell chromosome. The  
 CC excessive ovulation animal is useful for improving the productivity of  
 CC animals. The method can improve the productivity of a useful animal.  
 SQ Sequence 1295 AA;  
 Query Match 91.4%; Score 1282; DB 20; Length 1295;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MATQKASDERSIQPDHNLPELSALLGLDAVOLAKELSEEBOKERAMQGYNSOMRSE 60  
 Db 1 MATQKASDERSIQPDHNLPELSALLGLDAVOLAKELSEEBOKERAMQGYNSOMRSE 60  
 QY 61 AKRLKFTVYBEPYSSWIPQEMAAAGFYFTGVKSGIQPCCSLILFGAGLTRPLEDHKRF 120  
 Db 61 AKRLKFTVYBEPYSSWIPQEMAAAGFYFTGVKSGIQPCCSLILFGAGLTRPLEDHKRF 120  
 QY 121 HPDCGFLNKDVGNAKTDIRYKQLKSLRGKRYOEEERARLASPNMPPYVQGISPCV 180  
 Db 121 HPDCGFLNKDVGNAKTDIRYKQLKSLRGKRYOEEERARLASPNMPPYVQGISPCV 180  
 QY 181 LSEAGFVLTGQDPTVQCSGCGCLGNMBEGDPWKERAKVFPKCEPLRSKSSSEITQYI 240  
 Db 181 LSEAGFVLTGQDPTVQCSGCGCLGNMBEGDPWKERAKVFPKCEPLRSKSSSEITQYI 240  
 QY 241 OSYKGFVDITGEHFNVSQRELPMASAYCNDSTFAVEELRLSPQDNPRESAVGAALA 300  
 Db 241 OSYKGFVDITGEHFNVSQRELPMASAYCNDSTFAVEELRLSPQDNPRESAVGAALA 300  
 QY 301 KAGLFYTGIDIVQCFSCGCGCLEKMOEGDDPLDHTTRCPNCPFLQNMKSSAETVDPLOS 360  
 Db 301 KAGLFYTGIDIVQCFSCGCGCLEKMOEGDDPLDHTTRCPNCPFLQNMKSSAETVDPLOS 360

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QY 361 RGEICELLETSESNEEDSIAGPIVPEMAOGEAOWFOEAKNINLEOLRAAYTSASFRHNS 420
DB 361 RGEICELLETSESNEEDSIAGPIVPEMAOGEAOWFOEAKNINLEOLRAAYTSASFRHNS 420
QY 421 LLDISSDLATDHLGCDLSIASKHSKVPQEBVLVPEVFGNLSVMCEGEGSCKTVLL 480
DB 421 LLDISSDLATDHLGCDLSIASKHSKVPQEBVLVPEVFGNLSVMCEGEGSCKTVLL 480
QY 481 KIAIAPLMAAGCCPLNRFQVLYFVLSSTRPDEGLASII CDOLLEKESVTMCKRNIIQ 540
DB 481 KIAIAPLMAAGCCPLNRFQVLYFVLSSTRPDEGLASII CDOLLEKESVTMCKRNIIQ 540
QY 541 QUKNOVFLFLDDYKEICSIPOVIGKLIQGNHLSRTCLIAVTRNARDIRRLIETLLEIK 600
DB 541 QUKNOVFLFLDDYKEICSIPOVIGKLIQGNHLSRTCLIAVTRNARDIRRLIETLLEIK 600
QY 601 AFPYNTVCILRKLFSHNMTRLRKFMVYFGKQSLQKIOKTPLVAAICAHMFQYFPDPS 660
DB 601 AFPYNTVCILRKLFSHNMTRLRKFMVYFGKQSLQKIOKTPLVAAICAHMFQYFPDPS 660
QY 661 PDVAVFESYMERLSIRNKATAEILKATVSSCGELALKEFSCCEPENNDDLAEGVDED 720
DB 661 PDVAVFESYMERLSIRNKATAEILKATVSSCGELALKEFSCCEPENNDDLAEGVDED 720
QY 721 EDLTWCLMSKFTAOBLRPFYRFLSPAFOEFLAGMRLIELLSDROBODLGLYHLKOINS 780
DB 721 EDLTWCLMSKFTAOBLRPFYRFLSPAFOEFLAGMRLIELLSDROBODLGLYHLKOINS 780
QY 781 PMMTVSAVNNFLNYSVSLPSTAGPKIVSHLHLVDNKESENISENDDYLKHQPEISIQ 840
DB 781 PMMTVSAVNNFLNYSVSLPSTAGPKIVSHLHLVDNKESENISENDDYLKHQPEISIQ 840
QY 841 MGLAGLWICITCQAYFSWSEHLVLAALTAAYQSNVAAACSPVLOFLOGRTLTGALNL 900
DB 841 MGLAGLWICITCQAYFSWSEHLVLAALTAAYQSNVAAACSPVLOFLOGRTLTGALNL 900
QY 901 QYFFDHPESLILRSIHPIRGKNTSPRAHFSVLETCFPGKSOVPTIDODYASAFEMNEM 960
DB 901 QYFFDHPESLILRSIHPIRGKNTSPRAHFSVLETCFPGKSOVPTIDODYASAFEMNEM 960
QY 961 EBNLAKEEDNVKSYMDMORRASPDLSTGYMKLSPKOYKIPCLEVDVNDIDVVGOMLIEL 1020
DB 961 EBNLAKEEDNVKSYMDMORRASPDLSTGYMKLSPKOYKIPCLEVDVNDIDVVGOMLIEL 1020
QY 1021 MTFVFSASQIIEHLNHSRGFISIRPALHLSKASVTKCSISKLELSAAQOELLTLPSLE 1080
DB 1021 MTFVFSASQIIEHLNHSRGFISIRPALHLSKASVTKCSISKLELSAAQOELLTLPSLE 1080
QY 1081 SLEVASGTIOSODIPENLKFLCLKELSYDLEGNIVFSPVPEEPFNHMEKLIQISA 1140
DB 1081 SLEVASGTIOSODIPENLKFLCLKELSYDLEGNIVFSPVPEEPFNHMEKLIQISA 1140
QY 1141 EYDPSKLVKLIONSPNLHVFHLKCNFSDFGSLMTLVSCKLTEIKFSDFQAVPFA 1200
DB 1141 EYDPSKLVKLIONSPNLHVFHLKCNFSDFGSLMTLVSCKLTEIKFSDFQAVPFA 1200
QY 1201 SLPNFSLKILNLGEGQFPDEETSEKFAVILGSLSLLELILPTGGGIRVAKLIQQCC 1260
DB 1201 SLPNFSLKILNLGEGQFPDEETSEKFAVILGSLSLLELILPTGGGIRVAKLIQQCC 1260
QY 1261 OLHCLRVLSFFKTLNDSVVEI 1282
DB 1261 OLHCLRVLSFFKTLNDSVVEI 1282

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RESULT 8  
AA09540  
ID AA09540 standard; Protein; 1295 AA.

XX AA09540;  
XX 20-JUL-1999 (first entry)

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XX Human apoptosis inhibiting protein #2.
DE Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
XX Homo sapiens.
XX JPI116599-A.
XX 27-APR-1999.
XX 14-OCT-1997; 97JP-0280831.
XX 14-OCT-1997; 97JP-0280831.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 1999-323531/27.
XX N-PSDB; AAX56273.
XX New apoptosis inhibitory protein - useful for determining mechanism
XX of various apoptotic diseases e.g. human spinal muscular atrophy
XX Claim 1; Page 8-11; 16pp; Japanese.
XX The present sequence represents a human apoptosis inhibitory protein.
XX The apoptosis inhibitory protein is useful for the elucidation of
XX the mechanism of various apoptotic diseases such as human spinal
XX muscular atrophy and the diagnosis, the prevention and the treatment
XX of such diseases.
XX Sequence 1295 AA;
SQ
QY 1 MATOOKASDERISQPDHNLPELSALIGLDAVOLAKLEBBEROKERAMQKGYNSOMSE 60
DB 1 MATOOKASDERISQPDHNLPELSALIGLDAVOLAKLEBBEROKERAMQKGYNSOMSE 60
QY 61 AKRLKTPVTEYBYSWIMIOEMAAGFTGYVSGIQCFCCSLILFGAGILTRLPIDHGRF 120
DB 61 AKRLKTPVTEYBYSWIMIOEMAAGFTGYVSGIQCFCCSLILFGAGILTRLPIDHGRF 120
QY 121 HPDCGFLINKDVGNIATYDIRVKNLSKRLRGKMYQEEBARLASFRNMPFYVQGISPCV 180
DB 121 HPDCGFLINKDVGNIATYDIRVKNLSKRLRGKMYQEEBARLASFRNMPFYVQGISPCV 180
QY 181 LSEAGFVFTGKODTVQCSGCGCLGNMEEGDDPMKEHAKWPKCFELRSKXSSEETIYI 240
DB 181 LSEAGFVFTGKODTVQCSGCGCLGNMEEGDDPMKEHAKWPKCFELRSKXSSEETIYI 240
QY 241 QSYKGFVDITGEHFNYSWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGVALA 300
DB 241 QSYKGFVDITGEHFNYSWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGVALA 300
QY 301 KAGLFYTGIKDITVQCFSCGCGCLERKQEGDDPLDHTRCPCNCPYQNNKSSAEVTPDIOS 360
DB 301 KAGLFYTGIKDITVQCFSCGCGCLERKQEGDDPLDHTRCPCNCPYQNNKSSAEVTPDIOS 360
QY 361 RGEICELLETSESNEEDSIAGPIVPEMAOGEAOWFOEAKNINLEOLRAAYTSASFRHNS 420
DB 361 RGEICELLETSESNEEDSIAGPIVPEMAOGEAOWFOEAKNINLEOLRAAYTSASFRHNS 420
QY 421 LLDISSDLATDHLGCDLSIASKHSKVPQEBVLVPEVFGNLSVMCEGEGSCKTVLL 480
DB 421 LLDISSDLATDHLGCDLSIASKHSKVPQEBVLVPEVFGNLSVMCEGEGSCKTVLL 480
QY 481 KIAIAPLMAAGCCPLNRFQVLYFVLSSTRPDEGLASII CDOLLEKESVTMCKRNIIQ 540
DB 481 KIAIAPLMAAGCCPLNRFQVLYFVLSSTRPDEGLASII CDOLLEKESVTMCKRNIIQ 540

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QY	541	OLKQVLFLLDDYKEICSIPOVIGKLIQKHLSRTCLIAVTRNARAPRBYETIEIK	6000
Db	541	OLKQVLFLLDDYKEICSIPOVIGKLIQKHLSRTCLIAVTRNARAPRBYETIEIK <td>6000</td>	6000
QY	601	APFPYTVICILRLCFSHNMTRLRKEMVYGGKQSIQKIQKPLFVAALICAHMEQYPPDS	660
Db	601	APFPYTVICILRLCFSHNMTRLRKEMVYGGKQSIQKIQKPLFVAALICAHMEQYPPDS	660
QY	661	FDVVAIFKSYMERLSLRNKATAEILIKATVSSCGEIALKGFSSCFEENDDILAEAVDE	720
Db	661	FDVVAIFKSYMERLSLRNKATAEILIKATVSSCGEIALKGFSSCFEENDDILAEAVDE	720
QY	721	EDLTCLMSKFAQRLRPYRFLSPARPELAKGRLLLELDSROEHODIGLYHLMQINS	780
Db	721	EDLTCLMSKFAQRLRPYRFLSPARPELAKGRLLLELDSROEHODIGLYHLMQINS	780
QY	781	PMWTVSAYNNPFLNYVSLPSTKAGPKIVSHLLHVDNKESELENISENDYLRKHQPEISIQ	840
Db	781	PMWTVSAYNNPFLNYVSLPSTKAGPKIVSHLLHVDNKESELENISENDYLRKHQPEISIQ	840
QY	841	MQLRLGLMQLCPQAVFWSVSEHLVYLAKTAYQSNVYAACSPPVLOFLOGRTLTGALNT	900
Db	841	MQLRLGLMQLCPQAVFWSVSEHLVYLAKTAYQSNVYAACSPPVLOFLOGRTLTGALNT	900
QY	901	QYFPDHPSSLSLNSIHPPIRKGNKTSBRAHFSVLETCFDSQVPTIIDODYASAFEPNME	960
Db	901	QYFPDHPSSLSLNSIHPPIRKGNKTSBRAHFSVLETCFDSQVPTIIDODYASAFEPNME	960
QY	961	ERNLAEKEDNVKSYMDOQRASPDLSIGYWKLSPPQYKPLCLEVVDNDIDVVGQDMLEIL	1020
Db	961	ERNLAEKEDNVKSYMDOQRASPDLSIGYWKLSPPQYKPLCLEVVDNDIDVVGQDMLEIL	1020
QY	1021	MTVFSASQRIEHLNHSRGFIESIRPALEISKASVTKCSISKLELSAAEOELTLTBSLE	1080
Db	1021	MTVFSASQRIEHLNHSRGFIESIRPALEISKASVTKCSISKLELSAAEOELTLTBSLE	1080
QY	1081	SLEVSQTIQSQDQIFPNLDKFLCLKELSTDLEGNINVSVPPEEPNFHHEKLLIQISA	1140
Db	1081	SLEVSQTIQSQDQIFPNLDKFLCLKELSTDLEGNINVSVPPEEPNFHHEKLLIQISA	1140
QY	1141	EYPSKLVKLIONSPLVHFKCNFPDPSGLMTMLVSCKLTREKPSDSFOAVFPVA	1200
Db	1141	EYPSKLVKLIONSPLVHFKCNFPDPSGLMTMLVSCKLTREKPSDSFOAVFPVA	1200
QY	1201	SLPNFISLKLNLNEGQPPDETSKPAVYIIGSLNLEELPLPGDGIYAVAKLIQOQC	1260
Db	1201	SLPNFISLKLNLNEGQPPDETSKPAVYIIGSLNLEELPLPGDGIYAVAKLIQOQC	1260
QY	1261	QJHCURVLSFFKTLNDSVVEI	1282
Db	1261	QJHCURVLSFFKTLNDSVVEI	1282

FT	Misc-difference	919
XX	/note= "encoded by CCA"	
FN	MO9726331-A2.	
XX		
PD	24-JUL-1997.	
XX		
PF	17-JAN-1997; 97WO-IB00142.	
XX		
PR	19-JAN-1996; 96GB-0001108.	
PA	(UYOT-) UNIV OTTAWA.	
XX		
PI	Korneljuk RG, Mackenzie AE, Robertson G, Roy N, Tamai K,	
DR	WPI: 1997-38535/35.	
DR	N-PsDB; AAT71266.	
PT	New neuronal inhibitor of apoptosis - useful for diagnosing and	
FT	treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis	
PS	Claim 41; Fig 7A-L; 102pp; English.	
CC	Novel human neuronal apoptosis inhibitor protein (AAM20033), or NAIP,	
CC	is a negative regulator of apoptosis, partic. neuronal apoptosis	
CC	and, when deficient or absent, contributes to neurodegenerative	
CC	phenotypes such as spinal muscular atrophy (SMA) and amyotrophic	
CC	lateral sclerosis. Its amino acid sequence was deduced from a	
CC	cDNA clone (AAT71266) obtd. from a human foetal spinal cord cDNA	
CC	library. NAIP polypeptides, esp. those containing at least two	
CC	BIR (baculovirus IAP repeat) domains, can be expressed in host-	
CC	vector systems and used to increase or induce apoptosis for the	
CC	treatment of AIDS, neurodegenerative disease, myelodysplastic	
CC	syndromes or ischaemic injury, to screen for (anti)agonists, or to	
CC	produce antibodies useful for inhibiting apoptosis.	
XX		
SX	Sequence 1403 AA:	
QY	Query Match	
Db	Best Local Similarity 77.3%; Score 1084; DB 18; Length 1403;	
	Matches 1284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 MATQQASASDERISOPDHNLLPELSALLGLDAVOLAKELFEEOEKERAMQKGYNSOMRSE 60	
Db	1 MATQQAASDERISOPDHNLLPELSALLGLDAVOLAKELFEEOEKERAMQKGYNSOMRSE 60	
QY	61 ARRLTFPTYTEYSWSMIDPMAAAAGFYETGVSGIGQCSCSLIFGALITRLPIEDHKRF 120	
Db	61 ARRLTFPTYTEYSWSMIDPMAAAAGFYETGVSGIGQCSCSLIFGALITRLPIEDHKRF 120	
QY	121 HPDCGFLLANKOVGNIAKYDIVKNLKSRLRGSKRRYOBEERKLASFNNWPYYVGISPCV 180	
Db	121 HPDCGFLLANKOVGNIAKYDIVKNLKSRLRGSKRRYOBEERKLASFNNWPYYVGISPCV 180	
QY	181 LSEAGFVTGGQDTVOQCFSCGCGLANNBEGDPWKSHAKWPKCEFLRSKKSSBITOYT 240	
Db	181 LSEAGFVTGGQDTVOQCFSCGCGLANNBEGDPWKSHAKWPKCEFLRSKKSSBITOYT 240	
QY	241 QSYGAFPIDITEHNVNWMVORELPMSAYCNDISIFAYEELRLDSFKOMPRESAVGAVALA 300	
Db	241 QSYGAFPIDITEHNVNWMVORELPMSAYCNDISIFAYEELRLDSFKOMPRESAVGAVALA 300	
QY	301 KAGLFYTGINDIYOCFCSCGLEKMEOGDDPLDDHTRCFPNCFFLDNMKSSABVTPDIQS 360	
Db	301 KAGLFYTGINDIYOCFCSCGLEKMEOGDDPLDDHTRCFPNCFFLDNMKSSABVTPDIQS 360	
QY	361 RGEICELLETTSSNLSDSIANGVYPYEMAAQSEAOMFOBAKNLMDQLRAAYTSASFRRHS 420	
Db	361 RGEICELLETTSSNLSDSIANGVYPYEMAAQSEAOMFOBAKNLMDQLRAAYTSASFRRHS 420	
QY	421 LLDISSDLATDHLLGCDLSIASKHISKIPVOEPLVPEVNGNINSMVCVEGEGSGKTLYL 480	
Db	421 LLDISSDLATDHLLGCDLSIASKHISKIPVOEPLVPEVNGNINSMVCVEGEGSGKTLYL 480	



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QY 481 KKIATLWASGCCPLNRFQVLYSLSTRPDEGLASIIICDQLEKEGSEVTEMCNRIIQ 540
DB 481 KKIATLWASGCCPLNRFQVLYSLSTRPDEGLASIIICDQLEKEGSEVTEMCNRIIQ 540
QY 541 QLKNOVLFLDDYKKEICSIPOYIGKLIQKHLSTRCLLIANTNARDIRRLLEITLLEIK 600
DB 541 QLKNOVLFLDDYKKEICSIPOYIGKLIQKHLSTRCLLIANTNARDIRRLLEITLLEIQ 600
QY 601 APPFNVTICLRKLSHNTLRKFMVYVYGNOSLOKIOKTPLEVAICAHMFOYPPDS 660
DB 601 APPFNVTICLRKLSHNTLRKFMVYVYGNOSLOKIOKTPLEVAICAHMFOYPPDS 660
QY 661 PDDVAVFKSYMERLSIRNKATAIILKATVSSCGELALNGFSCCEFEFDDDLAAGVDED 720
DB 661 PDDVAVFKSYMERLSIRNKATAIILKATVSSCGELALNGFSCCEFEFDDDLAAGVDED 720
QY 721 EDLTWCLMSKFTAQRLRPYRFLSPAFOFLAGMRLIELLSDROHODLGLYHLKOINS 780
DB 721 EDLTWCLMSKFTAQRLRPYRFLSPAFOFLAGMRLIELLSDROHODLGLYHLKOINS 780
QY 781 PMMTVSAYNNELANYVSLPSTKAGPKIVSHLHLVDNKSLENISENDYILKHQPEISIQ 840
DB 781 PMMTVSAYNNELANYVSLPSTKAGPKIVSHLHLVDNKSLENISENDYILKHQPEISIQ 840
QY 841 MOLLGLMOICPOAFVSMVSEHLVLALKTAYQSNVVAACSPVLOFLQRTTLGALNTL 900
DB 841 MOLLGLMOICPOAFVSMVSEHLVLALKTAYQSNVVAACSPVLOFLQRTTLGALNTL 900
QY 901 QYFDPHPSLSLRSIHPIRGNKTSPPRAHFSVLETCPDKSOVPTIDODYASAFEBNEM 960
DB 901 QYFDPHPSLSLRSIHPIRGNKTSPPRAHFSVLETCPDKSOVPTIDODYASAFEBNEM 960
QY 961 EBNLAEKENVNSYMDMORASPDLSGTWKLSPKQYKPCLEVDVNDIDVQODMLETL 1020
DB 961 EBNLAEKENVNSYMDMORASPDLSGTWKLSPKQYKPCLEVDVNDIDVQODMLETL 1020
QY 1021 MTFVFSASQRIEHLNHSRGFIESIRPALBELSKASVTKCSISKLELSAAQOELLTLPSLE 1080
DB 1021 MTFVFSASQRIEHLNHSRGFIESIRPALBELSKASVTKCSISKLELSAAQOELLTLPSLE 1080
QY 1081 SLEVSCTTIOSODQIFPNLDKFLCKELSYDLBGNINVFVIBEFPFHMEKLLIQISA 1140
DB 1081 SLEVSCTTIOSODQIFPNLDKFLCKELSYDLBGNINVFVIBEFPFHMEKLLIQISA 1140
QY 1141 EYDPSKLVKLQNSPMLHVFHLKCNFPDGSMTMLVSCKLTETKFSDFQAVPFA 1200
DB 1141 EYDPSKLVKLQNSPMLHVFHLKCNFPDGSMTMLVSCKLTETKFSDFQAVPFA 1200
QY 1201 SLPNFSLKILNLEGOFPDEETSEKFAIYIGLSLSELIILPTGDIYRVAKLIIQOCO 1260
DB 1201 SLPNFSLKILNLEGOFPDEETSEKFAIYIGLSLSELIILPTGDIYRVAKLIIQOCO 1260
QY 1261 QHCLRVLSFPKTLNDSVVEIAKVA 1286
DB 1261 QHCLRVLSFPKTLNDSVVEIAKVA 1286

```

## RESULT 10

AA98217  
ID AA98217 standard; Protein; 1232 AA.

AA98217;

30-DEC-1996 (first entry)

Neuronal apoptosis inhibiting protein.

Neuronal apoptosis inhibiting protein; human; NAIp; chromosome 5q13; YAC;

yeast artificial chromosome; spinal muscular atrophy; mammalian cell; SMA;

autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA;

spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism.

```

OS Homo sapiens.
XX WO9612016-A1.
PN 25-APR-1996.
XX 17-OCT-1995; 95WO-CA00581.
XX 19-DEC-1994; 94CA-2138425.
PR 18-OCT-1994; 94GB-0021019.
XX (SHKJ) RDS DEV CORP JAPAN.
PA (UYOT-) UNITV OTTAWA.
XX Ikeda J, Korneluk RG, Mackenzie AB, Mahadevan MS;
XX McLean M, Roy N;
XX WPI, 1996-222003/22.
XX N-PSDB; AAT30092.
XX Neutonal apoptosis inhibitor protein gene - used to develop prods.
XX for use in the diagnosis and therapy of spinal muscular atrophy
XX Claim 3; Page 68-70; 113pp; English.
XX
XX This sequence represents the human neuronal apoptosis inhibitor protein
XX (NAIP). The cDNA encoding this sequence was found on a region of the
XX human chromosome 5q13. This sequence was isolated from a yeast
XX artificial chromosome (YAC) contig containing the D5S435-D5S112 interval
XX of the chromosome 5q13. Mutations in the NAIP gene, are causative of
XX spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of
XX autosomal recessive, neurodegenerative disorders. SMAs are classified
XX into the three types based upon the age of onset (with type I being the
XX severest form with the earliest age of onset). All three types are
XX characterised by the degeneration of the alpha motor neurons of the
XX spinal cord manifesting as weakness and wasting of the proximal voluntary
XX muscles. The most common mutations of the NAIP gene sequence are thought
XX to be deletions of exons 5 and 6, and reductions in the copy number of
XX the gene. The NAIP gene, (and primers and probes based on it) can be
XX used for the diagnosis of SMA, and for directing the formulation of
XX conventional and genetic therapies for SMA. Identification of genes
XX showing homology with the NAIP locus, and proteins that interact with
XX CC NAIP can be used in the elucidation of apoptotic mechanisms in mammalian
XX cells.
XX
XX Sequence 1232 AA:
XX
XX Query Match 67.4%; Score 946; DB 17; Length 1232;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1146; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 MATOQKASPERISQPDHMLPLSLALLGIDAVOLAKELBEEBOKRAXKQKYNQMSSE 60
DB 1 MATOQKASPERISQPDHMLPLSLALLGIDAVOLAKELBEEBOKRAXKQKYNQMSSE 60
QY 61 AKRLKTPVYBPSYSSNIPQEMAAAGFYFTGVNSGICQPCCSILFGAGLTRPIEDHKRF 120
DB 61 AKRLKTPVYBPSYSSNIPQEMAAAGFYFTGVNSGICQPCCSILFGAGLTRPIEDHKRF 120
QY 121 HPDCGFLINKDVGNIATKYDIRVKNLKSRLGKGMRYOBEARILASFRMPPYVOGISPCV 180
DB 121 HPDCGFLINKDVGNIATKYDIRVKNLKSRLGKGMRYOBEARILASFRMPPYVOGISPCV 180
QY 181 LSBAGFVFTGKODTVQCSGCGCLGNWEGDDPMKBAKMFCKCEFLSKSSSEITQYI 240
DB 181 LSBAGFVFTGKODTVQCSGCGCLGNWEGDDPMKBAKMFCKCEFLSKSSSEITQYI 240
QY 241 QSYKGFVDITGSHFNSWQRELPMASAYCNDISIFAYEELRIDSFPDMPRESAVGAALA 300
DB 241 QSYKGFVDITGSHFNSWQRELPMASAYCNDISIFAYEELRIDSFPDMPRESAVGAALA 300
QY 301 KAGLFYTGKIDIVOCFSCGCLKQBGDDPLDDHTRCPPNCPLONMKSAEVTPIQGS 360
DB 301 KAGLFYTGKIDIVOCFSCGCLKQBGDDPLDDHTRCPPNCPLONMKSAEVTPIQGS 360

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Db      301 KAGLEFYTGIDIVOCFSCGCGCLEKWEQDDPLDHTGRCPNCPLOMKSAEVTPLDQS 360
Qy      361 RSELCELLTETTESNLEDSIAVGPVPMACGEAQMFEAQNLEQJPAATYASFRHMS 420
Db      361 RSELCELLTETTESNLEDSIAVGPVPMACGEAQMFEAQNLEQJPAATYASFRHMS 420
Qy      421 LLDISSDLDTHLACDLSIASKHISKEPQPLVPEVFGNLSVMCEBAGSGKTVLL 480
Db      421 LLDISSDLDTHLACDLSIASKHISKEPQPLVPEVFGNLSVMCEBAGSGKTVLL 480
Qy      481 KKIAPLMAAGCCPLNRFQVLYLSSTRPDEGLASIIDDLKEKGSVTENCKMNIIO 540
Db      481 KKIAPLMAAGCCPLNRFQVLYLSSTRPDEGLASIIDDLKEKGSVTENCKMNIIO 540
Qy      541 OLKQOVFLDDYKEICSIPOVIGKLIQKNHLSRTCLLAVRNRRARDIRRYETLLEIK 600
Db      541 OLKQOVFLDDYKEICSIPOVIGKLIQKNHLSRTCLLAVRNRRARDIRRYETLLEIK 600
Qy      601 AFPEYNTVCILRLKFSNNMTRLRKPMYREGNOSLOKIQKTPLEVAALCAHMFQYPPDS 660
Db      601 AFPEYNTVCILRLKFSNNMTRLRKPMYREGNOSLOKIQKTPLEVAALCAHMFQYPPDS 660
Qy      661 PDVAVKSYMERLSLRNKATAEILKATYSSCGELALKGFPSCCFEPNDDLAEGVDED 720
Db      661 PDVAVKSYMERLSLRNKATAEILKATYSSCGELALKGFPSCCFEPNDDLAEGVDED 720
Qy      721 EDLTMLMSKFTQORLPFRPLSPAPQEPFLAGMRLIELLDSROHDOLGLYHKKQINS 780
Db      721 EDLTMLMSKFTQORLPFRPLSPAPQEPFLAGMRLIELLDSROHDOLGLYHKKQINS 780
Qy      781 PMMTVAAYNNFLNLYVSSLPSTKAGPKIVSHLLVLDNKESENISENDYLRKHQPEISLQ 840
Db      781 PMMTVAAYNNFLNLYVSSLPSTKAGPKIVSHLLVLDNKESENISENDYLRKHQPEISLQ 840
Qy      841 MOLLRGLMOICPAQYAWSWSEHLVLAALKTAVQSTVAACSPVLOFLQGRITLTLGALNL 900
Db      841 MOLLRGLMOICPAQYAWSWSEHLVLAALKTAVQSTVAACSPVLOFLQGRITLTLGALNL 900
Qy      901 QYFPHPELSLRSIHPIRGNKTSPPAHFSVLETCDFKQOVTTIOOVYASAFEPNNEW 960
Db      901 QYFPHPELSLRSIHPIRGNKTSPPAHFSVLETCDFKQOVTTIOOVYASAFEPNNEW 960
Qy      961 EBNLEKEDNYSVMQMDORASPDLSCTGYWKLSPKQYKIPCLAEVDVNDIVVQODMLEIL 1020
Db      961 EBNLEKEDNYSVMQMDORASPDLSCTGYWKLSPKQYKIPCLAEVDVNDIVVQODMLEIL 1020
Qy      1021 MTFVSASQRIELHNSRGFIIESIRPALBELSKASVTKCSISKLELSAAEDELTLTPSLE 1080
Db      1021 MTFVSASQRIELHNSRGFIIESIRPALBELSKASVTKCSISKLELSAAEDELTLTPSLE 1080
Qy      1081 SLEVSCTIOSODQIFPVLDKFLCKELSVLEGNINVFVYIPEEPNPFHMERLILQISA 1140
Db      1081 SLEVSCTIOSODQIFPVLDKFLCKELSVLEGNINVFVYIPEEPNPFHMERLILQISA 1140
Qy      1141 EYDPSKLV 1148
Db      1141 EYDPSKLV 1148

```

## RESULT 11

AA053493 standard; Protein; 118 AA.

AA053493;

09-MAR-2001 (first entry)

Human colon cancer antigen protein sequence SEQ ID NO:1033.

Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytotoxic; cardiotoxic; neuroprotective; vulnary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; anti-infective; antibacterial; gene therapy; wound;

```

KW      neural disorder; immune system disorder; muscular disorder;
KW      reproductive disorder; gastrointestinal disorder; renal disorder;
KW      infectious disease; cardiovascular disorder.
OS      Homo sapiens.
XX      WO20005351-A1.
XX      21-SEP-2000.
XX      08-MAR-2000; 2000WO-US05863.
XX      12-MAR-1999; 99US-0124270.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Rosen CA, Ruben SM;
XX      WPI; 2000-587534/55.
XX      DR      N-PSDB; AAC98250.
XX      PT      Colon cancer associated gene sequences, referred to as colon cancer
XX      PT      antigens, useful for the treatment, prevention, and diagnosis of colon
XX      PT      disorders such as colon cancer.
XX      PS      Claim 11; Page 1612; 2104pp; English.
XX      AAC97991 to AAC98763 encode the human colon cancer associated proteins,
XX      CC      called human colon cancer antigens, given in AA053234 to AA054006. The
XX      CC      human colon cancer antigens can have cytotoxic, cardiotoxic, muscular;
XX      CC      neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
XX      CC      vulnary, nephrotropic, anti-infective and antibacterial activities, and
XX      CC      can be used in gene therapy. The colon cancer antigen polynucleotides,
XX      CC      treatment and antibodies to the proteins are useful for the prevention,
XX      CC      treatment and diagnosis of colon disorders, such as colon cancer. The
XX      CC      polynucleotides may be used in diagnostics and research, such as for
XX      CC      chromosome identification, and as hybridisation probes. The proteins
XX      CC      system disorders, muscular disorders, reproductive disorders,
XX      CC      gastrointestinal disorders, wounds, renal disorders, infectious
XX      CC      diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
XX      CC      AA054007 represent sequences used in the exemplification of the present
XX      CC      invention.
SQ      Sequence 118 AA;
Query Match
Best Local Similarity 5.3%; Score 75; DB 21; Length 118;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      607 TVCILRLKFSNNMTRLRKPMYREGNOSLOKIQKTPLEVAALCAHMFQYPPDSFDVAV 666
Db      1 TVCILRLKFSNNMTRLRKPMYREGNOSLOKIQKTPLEVAALCAHMFQYPPDSFDVAV 60
Qy      667 FKSYMERLSLRNKAT 681
Db      61 FKSYMERLSLRNKAT 75

```

## RESULT 12

AA01849 standard; Protein; 60 AA.

AA01849;

06-OCT-2000 (first entry)

Human secreted protein, SEQ ID NO: 5930.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.

```
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX N-PSDB; AAC01855.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 5930; 71bp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
XX of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
XX were prepared from total human RNAs or polyA+ RNAs derived from 30
XX different tissues. EST sequences usually correspond mainly to the 3'
XX untranslated region (UTR) of the mRNA because they are often obtained
XX from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
XX isolating cDNA sequences derived from the 5' ends of mRNAs and even in
XX those cases where longer cDNA sequences have been obtained, the full 5'
XX UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
XX ends and can therefore be used to obtain full length cDNAs with intact
XX DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
XX chromosome mapping procedures. They are used to obtain upstream
XX regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 60 AA;
XX
XX Query Match 4.3%; Score 60; DB 21; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-53;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 265 MASAYCNDISFAYEELRLDSFKDMPRESAVGVAAALAKGLFTYIGDIYQCFSCGGLER 324
XX 1 MASAYCNDISFAYEELRLDSFKDMPRESAVGVAAALAKGLFTYIGDIYQCFSCGGLER 60
XX
XX RESULT 13
XX AAO12411
XX ID AAO12411 standard; Protein; 51 AA.
XX
XX AAO12411;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 26303.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
XX
XX 28-FEB-2000; 2000US-0515126.
XX
XX 18-MAY-2000; 2000US-0577409.
XX
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```
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX N-PSDB; AA192342.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX
XX Claim 20; SEQ ID NO 26303; 1399bp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AA000010-AA013910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 51 AA;
XX
XX Query Match 1.8%; Score 25; DB 22; Length 51;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-17;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 224 CEPLRSKKSSEITQYIOSYKGFVD 248
XX 10 CEPLRSKKSSEITQYIOSYKGFVD 34
XX
XX RESULT 14
XX ABG55972
XX ID ABG55972 standard; Peptide; 37 AA.
XX
XX ABG55972;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver peptide, SEQ ID NO 34620.
XX
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00664.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488898/53.
XX
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XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human adult liver
XX
PS Claim 27; SEQ ID No 34620; 658bp; English.
CC The invention relates to a single exon nucleic acid probe (SNP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (1) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABG47348-ABG5930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 SKKSEETIQTYSYKGFVDIT 250
DB 1 SKKSEETIQTYSYKGFVDIT 22

RESULT 15
AAM74180
ID AAM74180 standard; Protein; 37 AA.
XX
AC AAM74180;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34466.
XX
KM Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
OS Homo sapiens.
XX
PV MO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 34486; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid

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CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention.
SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 SKKSEETIQTYSYKGFVDIT 250
DB 1 SKKSEETIQTYSYKGFVDIT 22

RESULT 16
AAM34307
ID AAM34307 standard; Protein; 37 AA.
XX
AC AAM34307;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #8344 encoded by probe for measuring placental gene expression.
XX
KM Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
OS Homo sapiens.
XX
PV MO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488997/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 27; SEQ ID No 34576; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SNP:
CC see A13315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
SQ Sequence 37 AA;

Query Match 1.6%; Score 22; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 SKKSEETIQTYSYKGFVDIT 250
DB 1 SKKSEETIQTYSYKGFVDIT 22

```

RESULT 17  
 ABG44119  
 ID ABG44119 standard; Peptide; 37 AA.  
 XX  
 AC ABG44119;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 33784.  
 XX  
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00665.  
 XX  
 PR 04-FEB-2000; 2000US-180312P.  
 PR 26-MAY-2000; 2000US-207456P.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-234687P.  
 PR 27-SEP-2000; 2000US-236359P.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 XX measure gene expression in human lung samples -  
 XX  
 PS Claim 27; SEQ ID NO 33784; 634pp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of  
 CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberosus sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hereditary-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 37 AA;  
 XX  
 Query Match 1.6%; Score 22; DB 23; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-14;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 229 SKKSEBITOYIQSYKGFVDIT 250  
 DB 1 SKKSEBITOYIQSYKGFVDIT 22  
 XX  
 RESULT 18  
 AA006778  
 ID AA006778 standard; Protein; 67 AA.  
 XX  
 AC AA006778;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 20670.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200164835-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US04927.  
 XX  
 PR 28-FEB-2000; 2000US-0515126.  
 PR 18-MAY-2000; 2000US-0577409.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-514838/56.  
 DR N-PSDB; AA186709.  
 XX  
 PT Isolated nucleic acids and polypeptides, useful for preventing  
 PT diagnosing and treating e.g. leukaemia, inflammation and immune  
 PT disorders -  
 XX  
 PS Claim 20; SEQ ID NO 20670; 1399pp + Sequence Listing; English.  
 XX  
 CC The invention relates to human polynucleotides (AA179941-AA193841) and  
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activity/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 67 AA;  
 Query Match 0.6%; Score 9; DB 22; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1377 MKERHPOSK 1385  
 DB 41 MKERHPOSK 49  
 RESULT 19  
 ID ABB81447 standard; Protein: 210 AA.  
 AC ABB81447;  
 XX  
 DT 04-MAR-2003 (first entry)  
 DE Streptococcus pneumoniae polypeptide SEQ ID NO 364.  
 XX  
 KM Streptococcus pneumoniae; infection; otitis media; antibacterial;  
 XX diagnosis; gene therapy.  
 XX Streptococcus pneumoniae.  
 XX WO200283855-A2.  
 XX  
 PD 24-OCT-2002.  
 PF 12-APR-2002; 2002WO-US11524.  
 XX  
 PR 16-APR-2001; 2001US-283948P.  
 PR 18-APR-2001; 2001US-284443P.  
 XX  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Zagursky RJ, Masi AW, Green BA, Chakravarti DN, Russell DP;  
 PI Woelers JL;  
 XX  
 DR WPI, 2003-093010/08.  
 DR N-PSDB; AB242295.  
 XX  
 PT New Streptococcus pneumoniae polynucleotides, useful for treating or  
 PT preventing S. pneumoniae infections, or non-systemic diseases, e.g.,  
 PT otitis media, which are induced or exacerbated by S. pneumoniae -  
 PS Claim 42; Page 599-600; 1091pp; English.  
 XX  
 CC The invention relates to isolated polynucleotides (AB272147-AB242522) of  
 CC a Streptococcus pneumoniae genomic sequence, a fragment or degenerate  
 CC variant of the polynucleotide or a nucleic acid sequence 95% identical to  
 CC one of the polynucleotides. The S. pneumoniae polynucleotides and  
 CC encoded polypeptides (ABP81299-ABP81674) are useful for treating or  
 CC preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis  
 CC media, which are induced or exacerbated by S. pneumoniae. These are also  
 CC useful for detecting S. pneumoniae in a biological sample or diagnosing  
 CC S. pneumoniae infection in a subject. The polynucleotides have  
 CC antibacterial activity and are useful in gene therapy.  
 XX  
 SQ Sequence 210 AA;  
 Query Match 0.6%; Score 9; DB 24; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 473 GSGKTVLTK 481  
 DB 38 GSGKTVLTK 46  
 RESULT 20  
 ID ABOU2180 standard; Protein: 210 AA.  
 XX  
 AC ABOU2180;  
 XX  
 DT 11-FEB-2003 (first entry)  
 DE S. pneumoniae type 4 strain protein from coding region #1757.  
 XX  
 KM Bacterial meningitis; pneumonia; sepsis; otitis media;  
 KM ear infection; antiinflammatory; antibacterial; immunostimulant;  
 KM auditory; respiratory; gene therapy; vaccine.  
 XX  
 OS Streptococcus pneumoniae type 4 strain.  
 XX  
 PN WO200277021-A2.  
 XX  
 PD 03-OCT-2002.  
 PF 27-MAR-2002; 2002WO-IB02163.  
 XX  
 PR 27-MAR-2001; 2001GB-0007658.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Masignani V, Tettelin H, Fraser C;  
 XX  
 DR WPI, 2003-040579/03.  
 DR N-PSDB; ABX07469.  
 XX  
 PT New proteins and nucleic acid molecules from Streptococcus pneumoniae,  
 PT useful as medicaments for treating or preventing a disease or infection  
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media  
 PT or ear infection -  
 PS Claim 1; SEQ ID NO 3514; 56pp; English.  
 XX  
 CC The invention relates to a protein comprising or having at least 50%  
 CC identity to any of the 2469 amino acid sequences, identified in the  
 CC specification (available on a computer readable format), or its fragment,  
 CC expressed from 2469 of 2489 identified DNA coding regions from the  
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as  
 CC ABS56454. Also included are an antibody which binds one of the  
 CC proteins, treating a patient by administering the protein, DNA or  
 CC antibody (in a composition), a kit comprising first and second primers,  
 CC which are the nucleic acid cited above or fragments between nucleotides  
 CC 8-100 of a sequence not defined in the specification, for amplifying a  
 CC target sequence contained within a Streptococcus nucleic acid sequence,  
 CC where the first primer is substantially complementary to the target  
 CC sequence and the second primer is substantially complementary to the  
 CC complement of the target sequence, and where the parts of the primers  
 CC having substantial complementarity define the termini of the target  
 CC sequence to be amplified, assay comprising contacting a test compound  
 CC with the protein, and determining whether the test compound binds to the  
 CC protein and a Streptococcus pneumoniae bacterium, where one or more  
 CC genes encoding the proteins has been rendered inactive. The proteins,  
 CC nucleic acid molecules, antibody and compositions are useful as  
 CC medicaments for treating or preventing a disease or infection due to  
 CC streptococcus bacteria, particularly S. pneumoniae, such as pneumonia,  
 CC sepsis, otitis media or ear infection. They are also useful in developing  
 CC vaccines, diagnostics and antibiotics. The methods are useful for  
 CC identifying immunodominant proteins. The present sequence is one of  
 CC the 2469 proteins expressed by the identified coding regions from the  
 CC genomic sequence.

CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pat\_sequences.

**SQ Sequence 210 AA;**

Query Match	0.6%	Score 9;	DB 24;	Length 210;
Best Local Similarity	100.0%	Pred. No. 4.1;		
Matches	9;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

```

Oy      473 GSGKTVLLK 481
         |||||
Db      38  GSGKTVLLK 46

```

RESULT 21  
AAG28074

AC AAG28074;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 33155

KM Protein identification; signal transduction pathway; metabolic pathway;  
 KM hybridisation assay; genetic mapping; gene expression control; promoter;  
 KM termination sequence.

OS *Arabidopsis thaliana*

PN EP1033405-A2

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439

PR	25-FEB-1999	9905-0121825
PR	05-MAR-1999	9905-0123180
PR	05-MAR-1999	9905-0123180
PR	09-MAR-1999	9905-0123548
PR	23-MAR-1999	9905-0125788
PR	25-MAR-1999	9905-0126264
PR	29-MAR-1999	9905-0126785
PR	01-APR-1999	9905-0127462
PR	06-APR-1999	9905-0128234
PR	08-APR-1999	9905-0128714
PR	15-APR-1999	9905-0129865
PR	19-APR-1999	9905-0130077
PR	21-APR-1999	9905-0130049
PR	23-APR-1999	9905-0130510
PR	23-APR-1999	9905-0130851
PR	28-APR-1999	9905-0131449
PR	30-APR-1999	9905-0133048
PR	30-APR-1999	9905-0133407
PR	04-MAY-1999	9905-0133484
PR	05-MAY-1999	9905-0133485
PR	06-MAY-1999	9905-0133487
PR	06-MAY-1999	9905-0133487
PR	07-MAY-1999	9905-0133863
PR	11-MAY-1999	9905-0134256
PR	14-MAY-1999	9905-0134218
PR	14-MAY-1999	9905-0134219
PR	14-MAY-1999	9905-0134221
PR	14-MAY-1999	9905-0134370
PR	18-MAY-1999	9905-0134768
PR	19-MAY-1999	9905-0134941
PR	20-MAY-1999	9905-0135124
PR	21-MAY-1999	9905-0135553
PR	24-MAY-1999	9905-0135629
PR	25-MAY-1999	9905-0136021
PR	27-MAY-1999	9905-0136392
PR	28-MAY-1999	9905-0136582

PR	03-JUN-1999	99US-01377222
PR	03-JUN-1999	99US-01375728
PR	04-JUN-1999	99US-01375702
PR	07-JUN-1999	99US-01377724
PR	08-JUN-1999	99US-01380944
PR	10-JUN-1999	99US-01385470
PR	10-JUN-1999	99US-01388440
PR	14-JUN-1999	99US-01391119
PR	16-JUN-1999	99US-01394522
PR	16-JUN-1999	99US-01394543
PR	17-JUN-1999	99US-01394942
PR	18-JUN-1999	99US-01394954
PR	18-JUN-1999	99US-01394545
PR	18-JUN-1999	99US-01394558
PR	18-JUN-1999	99US-01394557
PR	18-JUN-1999	99US-01394577
PR	18-JUN-1999	99US-01394589
PR	18-JUN-1999	99US-01394598
PR	18-JUN-1999	99US-01394603
PR	18-JUN-1999	99US-01394621
PR	18-JUN-1999	99US-01394662
PR	18-JUN-1999	99US-01394663
PR	18-JUN-1999	99US-01397500
PR	18-JUN-1999	99US-01400523
PR	18-JUN-1999	99US-01400695
PR	20-JUN-1999	99US-01402930
PR	20-JUN-1999	99US-01405991
PR	20-JUN-1999	99US-01412877
PR	20-JUN-1999	99US-01418442
PR	20-JUN-1999	99US-01421544
PR	20-JUN-1999	99US-01420555
PR	20-JUN-1999	99US-01423900
PR	20-JUN-1999	99US-01428203
PR	09-JUL-1999	99US-01442920
PR	12-JUL-1999	99US-01442937
PR	12-JUL-1999	99US-01443342
PR	14-JUL-1999	99US-01435244
PR	15-JUL-1999	99US-01440055
PR	16-JUL-1999	99US-01440885
PR	16-JUL-1999	99US-01440866
PR	19-JUL-1999	99US-01444325
PR	19-JUL-1999	99US-01444331
PR	19-JUL-1999	99US-01444332
PR	19-JUL-1999	99US-01444333
PR	19-JUL-1999	99US-01444334
PR	19-JUL-1999	99US-01444335
PR	20-JUL-1999	99US-01444352
PR	20-JUL-1999	99US-01444353
PR	20-JUL-1999	99US-01444354
PR	20-JUL-1999	99US-01444884
PR	21-JUL-1999	99US-01444814
PR	21-JUL-1999	99US-01450806
PR	21-JUL-1999	99US-01450808
PR	21-JUL-1999	99US-01450888
PR	22-JUL-1999	99US-01450879
PR	22-JUL-1999	99US-01450887
PR	22-JUL-1999	99US-01451592
PR	22-JUL-1999	99US-01451545
PR	23-JUL-1999	99US-01451548
PR	23-JUL-1999	99US-01451524
PR	23-JUL-1999	99US-01455766
PR	26-JUL-1999	99US-01455726
PR	27-JUL-1999	99US-01455183
PR	27-JUL-1999	99US-01455113
PR	27-JUL-1999	99US-01455219
PR	28-JUL-1999	99US-01455521
PR	02-AUG-1999	99US-01465886
PR	02-AUG-1999	99US-01465888
PR	02-AUG-1999	99US-01465898
PR	03-AUG-1999	99US-01470308
PR	04-AUG-1999	99US-01477204
PR	04-AUG-1999	99US-01477202

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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 07-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152363.
PR 13-SEP-1999; 99US-0153070.
PR 15-SEP-1999; 99US-0153758.
PR 16-SEP-1999; 99US-0154018.
PR 20-SEP-1999; 99US-0154039.
PR 22-SEP-1999; 99US-0154779.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 29-SEP-1999; 99US-0156458.
PR 04-OCT-1999; 99US-0156596.
PR 05-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0157865.
PR 08-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158232.
PR 13-OCT-1999; 99US-0158359.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 0.6%; Score 9; DB 21; Length 341;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LAKELESEE 42
Db 95 LAKELESEE 103

RESULT 22
AAB65694
ID AAB65694 standard; Protein; 349 AA.
XX
AC AAB65694;
XX
DE 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 222.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Mus musculus.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14842.
XX
PR 28-MAY-1999; 99US-0136503.
XX
PA (SUGR-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
XX
DR N-PSDB; AAF4722.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
PS Claim 10; Fig 1; 310pp; English.
XX
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
XX
SQ Sequence 349 AA;

```

Query Match 0.6%; Score 9; DB 22; Length 349;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1231 LGSLSNLEB 1239  
 DB 153 LGSLSNLEB 161

## RESULT 23

AAU03542  
 ID AAU03542 standard; Protein; 350 AA.

AC AAU03542;

DT 12-SEP-2001 (first entry)

DE Human protein kinase #42.

DE Human; protein kinase; PTK; STK; cancer; cardiovascular disease;

KW metabolic disorder; immune related disease; neurological disorder;

KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW reproductive disorder.

OS Homo sapiens.

PN WO200138503-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US32085.

PR 24-NOV-1999; 99US-0167482.

PA (SUGEN-) SUGEN INC.

PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI Flanagan P, Clary D;

DR WPI; 2001-343950/36.

DR N-PSDB; AAS06742.

XX Nucleic acids encoding human kinase polypeptides, useful for preventing

PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and

PT neuronal-associated diseases, and microbial infections -

PS Claim 7; Figure 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The

CC novel protein kinases have been identified as members of the tyrosine

CC or serine/threonine kinase (PTK and STK) families. The polynucleotides

CC encoding protein kinases and the polypeptides may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate kinase expression. For example, they may be used to treat

CC cancers (especially cancers of hematopoietic origin), cardiovascular

CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

CC immune related diseases (e.g. rheumatoid arthritis), neurological

CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.

CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious

CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

CC Additionally, polynucleotides encoding protein kinases may be

CC used for gene therapy and as DNA probes in diagnostic assays.

CC The protein kinase polypeptides may be used as antigens in the production

CC of antibodies against the protein kinases and in assays to identify

CC modulators of protein kinase expression and activity.

XX Sequence 350 AA;

XX SQ

XX Query Match 0.6%; Score 9; DB 22; Length 350;

XX Best Local Similarity 100.0%; Pred. No. 6.8;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1231 LGSLSNLEB 1239

XX DB 154 LGSLSNLEB 162

RESULT 24  
 ABP69792  
 ID ABP69792 standard; Protein; 350 AA.

AC ABP69792;

DT 20-JAN-2003 (first entry)

DE Human polypeptide SEQ ID NO 1839.

DE Human; genome mapping; gene therapy; food supplement; virus; fungus;

KW cell-proliferative disorder; neurodegenerative disease; bacterial;

KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

KW arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;

KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;

KW antiarthritic.

OS Homo sapiens.

PN WO200270539-A2.

PD 12-SEP-2002.

PF 05-MAR-2002; 2002WO-US05095.

PR 05-MAR-2001; 2001US-0799451.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao Q, Ren F;

PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

PI Wehrman T, Wang J, Wang D, Drmanac RT;

DR WPI; 2002-759612/82.

DR N-PSDB; AB212009.

XX New polynucleotides comprising sequences assembled from expressed

PT sequence tags (ESTs), useful for treating cell-proliferative,

PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or

PT platelet or coagulation disorders -

PS Claim 9; SEQ ID NO 1839; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (1) comprising a

CC nucleotide sequence selected from any of 948 sequences

CC (AB211119-AB212066) or their mature protein coding portion, active domain

CC coding protein or complementary sequences. The polynucleotides are useful

CC for identifying expressed genes or for physical mapping of human genome.

CC The encoded polypeptides (ABP6902-ABP6949) are useful as molecular

CC weight markers, as a food supplement, for generating antibodies, in

CC medical imaging, screening and diagnostic assays and for treating

CC cell-proliferative disorders (cancer), neurodegenerative diseases

CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple

CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid

CC disorders, platelet or coagulation disorders, wound, burns, incision,

CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,

CC parasitic), arthritis, etc.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 350 AA;

XX SQ

XX Query Match 0.6%; Score 9; DB 22; Length 350;

XX Best Local Similarity 100.0%; Pred. No. 6.8;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1231 LGSLSNLEB 1239

XX DB 154 LGSLSNLEB 162

RESULT 25  
AAG28073  
ID AAG28073 standard; Protein; 416 AA.  
AC AAG28073;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33154.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
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DT 07-MAY-2002 (first entry)
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KW Human; proliferative disorder; tumor host range mutant virus; cancer;
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 DR WPI; 2001-483426/52.  
 XX N-PSDB; AAK56357.  
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 useful for preventing, diagnosing and/or treating cancers and

PT metastasis -  
 XX  
 XX Claim 11; SEQ ID NO 11169; 3071bp + Sequence listing; English.  
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 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cyclostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC protein and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC expression, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/hematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 56 AA;  
 QY 633 GSLQKIQK 640  
 DB 40 GSLQKIQK 47  
 RESULT 29  
 ABB50632  
 ID ABB50632 standard; Protein; 64 AA.  
 AC ABB50632;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 36 SEQ ID NO:580.  
 XX  
 KW Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;  
 KW dermatological; immunosuppressive; anti-inflammation; immunostimulant;  
 KW cytostatic; cardiac; vascular; anti-angiogenic; ophthalmological;  
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery;  
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;  
 KW Gaucher's disease; cardiovascular disease; scleroderma syndrome; chemotaxis;  
 KW Chagas's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;  
 KW corneal graft neovascularization; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease; chromosome 14.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162891-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PP 21-FEB-2001; 2001WO-US05614.  
 XX  
 XX 24-FEB-2000; 2000US-184836P.  
 PR 29-MAR-2000; 2000US-193170P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;  
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;  
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Fertie AM, Fan P,  
 PI Feng P, Endress CA, Dillon PJ, Carter KC, Brewer LA, Yu G;

PI Zeng Z, Greene JM;  
 XX MPI, 2001-625724/72.  
 DR  
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 PT  
 XX Disclosure; Page 85; 1533pp; English.  
 PS  
 XX  
 CC AAB50301 to AAB51287 and ABA8194 to ABA83441 represent human secreted  
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Example of these activities include: immunomodulatory; antisclerotic;  
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;  
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;  
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used  
 CC in gene therapy and vaccine production. (I) and (II) can be used in the  
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 CC Gaucher's disease), cardiovascular diseases (e.g. scintar syndrome,  
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic  
 CC disorders (e.g. corneal graft neovascularisation and diabetic  
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 CC ABA83193 and AAB50300 represent sequences used in the exemplification of  
 CC the present invention.  
 CC  
 XX  
 SQ Sequence 64 AA;

Query Match 0.6%; Score 8; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEOKER 46  
 |||||  
 DB 29 EEEOKER 36

RESULT 30  
 AAB54291

ID AAB54291 standard; Protein; 95 AA.

AC AAB54291;

DT 09-MAR-2001 (first entry)

DE Human pancreatic cancer antigen protein sequence SEQ ID NO:743.

XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
 KM detection; diagnosis; identification; cytostatic; neuroprotective;  
 KM nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;  
 KM antiinflammatory; cardiac; gene therapy; chromosome mapping;  
 KM linkage analysis; tissue identification; tissue typing; forensic;  
 KM neural; immune system; muscular; reproductive; gastrointestinal;  
 KM pulmonary; cardiovascular; renal; proliferative.

OS Homo sapiens.

PN WO200055320-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05989.

PR 12-MAR-1999; 99US-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

XX MPI, 2000-579444/54.  
 DR N-PSDB; AAC99056.  
 XX  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition -  
 PT  
 XX Claim 11; Page 1188; 1379pp; English.  
 PS  
 XX

CC AAC8773 to AAC9231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiac and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC9232 to AAC9240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 95 AA;

Query Match 0.6%; Score 8; DB 21; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1132 EKLIIQIS 1139  
 |||||  
 DB 37 EKLIIQIS 44

RESULT 31

ID AAU42144 standard; Protein; 113 AA.

AC AAU42144;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #3040.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KM dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PA (CORI-) CORIXA CORP.





PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144332.  
PR 20-JUL-1999; 99US-0144332.  
PR 20-JUL-1999; 99US-0144332.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145218.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145918.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149829.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151338.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154779.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155559.  
PR 28-SEP-1999; 99US-0156568.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.

PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 152;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 DEFTSEKF 1227  
DB 65 DEFTSEKF 72

RESULT 33  
AAG53555  
ID AAG53555 standard; Protein; 152 AA.  
XX  
AC AAG53555;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68195.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 18-MAY-1999; 99US-0134370.  
PR 19-MAY-1999; 99US-0134768.  
PR 20-MAY-1999; 99US-0134941.  
PR 21-MAY-1999; 99US-0135124.  
PR 24-MAY-1999; 99US-0135553.  
PR 25-MAY-1999; 99US-0135629.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0137804.  
PR 10-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 14-JUN-1999; 99US-0139847.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139761.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 26-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142803.  
PR 12-JUL-1999; 99US-0142920.  
PR 13-JUL-1999; 99US-0143277.  
PR 13-JUL-1999; 99US-0143642.  
PR 14-JUL-1999; 99US-0144005.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144332.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 23-JUL-1999; 99US-0145122.  
PR 23-JUL-1999; 99US-0145145.  
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PR 27-JUL-1999; 99US-0145313.  
PR 27-JUL-1999; 99US-0145318.  
PR 28-JUL-1999; 99US-0145319.  
PR 02-AUG-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0146389.  
PR 04-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 05-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 09-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 10-AUG-1999; 99US-0147935.  
PR 11-AUG-1999; 99US-0148171.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 16-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 18-AUG-1999; 99US-0149175.  
PR 20-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 23-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 25-AUG-1999; 99US-0149930.  
PR 26-AUG-1999; 99US-0150566.  
PR 27-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 30-AUG-1999; 99US-0151080.  
PR 31-AUG-1999; 99US-0151309.  
PR 01-SEP-1999; 99US-0151438.  
PR 07-SEP-1999; 99US-0151930.  
PR 10-SEP-1999; 99US-0152363.  
PR 13-SEP-1999; 99US-0153070.  
PR 15-SEP-1999; 99US-0153758.  
PR 16-SEP-1999; 99US-0154018.  
PR 20-SEP-1999; 99US-0154039.  
PR 22-SEP-1999; 99US-0154779.  
PR 23-SEP-1999; 99US-0155139.  
PR 24-SEP-1999; 99US-0155486.  
PR 28-SEP-1999; 99US-0155659.  
PR 29-SEP-1999; 99US-0156548.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.

PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 152;  
Best Local Similarity 100.0%; Pred. No. 33;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1220 DEETSEKF 1227  
|||||

Db 65 DEETSEKF 72

RESULT 34

AB61125  
ID AB61125 standard; Protein; 197 AA.

AC AB61125;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 10167.

KW Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL05228.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
genes from Drosophila and for elucidating cell signalling and cell-cell  
interactions -

PS Disclosure; SEQ ID NO 10167; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
capable of detecting 1000 or more genes from Drosophila. The invention is  
useful in developmental biology and in elucidating cell signalling and  
cell-cell interactions in higher eukaryotes for the development of  
insecticides, therapeutics and pharmaceutical drugs. The invention  
discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

CC sequences (AB101840-AB16175) and the encoded proteins  
CC (AB57737-AB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 197 AA;

Query Match 0.6%; Score 8; DB 22; Length 197;  
Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1384 SKYLTILQ 1391  
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Db 59 SKYLTILQ 66

RESULT 35

AA607151  
ID AA607151 standard; Protein; 232 AA.

AC AA607151;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 4193.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

KW Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134216.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134768.

PR 18-MAY-1999; 99US-0134941.

PR 19-MAY-1999; 99US-0135124.

PR 20-MAY-1999; 99US-0135133.

PR 21-MAY-1999; 99US-0135269.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782-  
PR 01-JUN-1999; 99US-0137222-  
PR 03-JUN-1999; 99US-0137528-  
PR 04-JUN-1999; 99US-0137502-  
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PR 25-AUG-1999; 99US-0149930-  
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PR 01-SEP-1999; 99US-0151330-  
PR 07-SEP-1999; 99US-0152363-  
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PR 28-OCT-1999; 99US-0161920-  
PR 28-OCT-1999; 99US-0161992-  
PR 28-OCT-1999; 99US-0161993-  
PR 29-OCT-1999; 99US-0162142-

Query Match 0.6%; Score 8; DB 21; Length 232;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1220 DETSEKF 1227  
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Db 145 DETSEKF 152

RESULT 36  
AAG53554  
ID AAG53554 standard; Protein; 232 AA.

AC AAG53554;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68194.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-01231825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

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PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 27-MAY-1999; 99US-0136021.

PR 28-MAY-1999; 99US-0136392.

PR 01-JUN-1999; 99US-0136782.

PR 03-JUN-1999; 99US-0137222.

PR 04-JUN-1999; 99US-0137528.

PR 07-JUN-1999; 99US-0137502.

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PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

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PR 18-JUN-1999; 99US-0139454.

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PR 18-JUN-1999; 99US-0139461.

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PR 18-JUN-1999; 99US-0139750.

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PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 28-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 30-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145087.

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PR 23-JUL-1999; 99US-0145145.

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PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 28-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

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PR 04-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

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PR 10-AUG-1999; 99US-0148171.  
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PR 17-AUG-1999; 99US-0149175.  
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PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
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PR 27-AUG-1999; 99US-0151080.  
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PR 01-SEP-1999; 99US-0151930.  
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PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 0.64; Score 8; DB 21; Length 232;  
Best Local Similarity 100.0%; Pred. No. 50;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 DEETSEKF 1227  
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DB 145 DEETSEKF 152  
RESULT 37  
AAG07150  
ID AAG07150 standard; Protein; 239 AA.  
XX AAG07150;  
AC  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4192.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD  
XX  
XX 06-SEP-2000.  
PF  
XX 25-FEB-2000; 2000EP-0301439.  
PR 25-FEB-1999; 99US-0123825.  
PR 05-MAR-1999; 99US-0123860.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
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PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142820.  
PR 12-JUL-1999; 99US-0142877.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
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PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
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PR 27-AUG-1999; 99US-0151080.  
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PR 01-SEP-1999; 99US-0151930.  
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PR 10-SEP-1999; 99US-0153070.  
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PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 239;  
Best Local Similarity 100.0%; Pred.No. 51;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1220 DBETSEKF 1227  
Db 152 DBETSEKF 159

RESULT 38  
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ID AAG53553 standard; Protein; 239 AA.  
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AC AAG53553;  
XX  
XX 18-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68193.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridization assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
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Query Match 0.6%; Score 8; DB 21; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 DEBTSEKF 1227  
 DB 152 DEBTSEKF 159

RESULT 39  
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 ID AAB53281 standard; Protein; 259 AA.  
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 AC AAB53281;  
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 DT 09-MAR-2001 (first entry)  
 XX  
 XX Human colon cancer antigen protein sequence SEQ ID NO:821.  
 XX  
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW identification; cytosolic; cardioactive; neuroprotective; vulnery;  
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
 KW nephrotoxic; antineoplastic; antibacterial; gene therapy; wound;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; renal disorder;  
 KW infectious disease; cardiovascular disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO20005351-A1.  
 XX  
 XX PD 21-SEP-2000.  
 XX  
 XX PF 08-MAR-2000; 2000MO-US05883.  
 XX  
 XX PR 12-MAR-1999; 99US-0124270.  
 XX  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX PI Rosen CA, Ruben SM;  
 XX  
 XX DR WPI. 2000-587534/55.  
 XX  
 XX DR N-PSDB; AAC98038.  
 XX  
 XX PT Colon cancer associated gene sequences, referred to as colon cancer  
 PT antigens, useful for the treatment, prevention, and diagnosis of colon  
 PT disorders such as colon cancer -  
 PS  
 XX Claim 11; Page 1374; 2104pp; English.  
 XX  
 XX PS AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
 CC called human colon cancer antigens, given in AAB5334 to AAB54006. The  
 CC human colon cancer antigens can have cytosolic, cardioactive, muscular;  
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
 CC vulnery, nephrotoxic, antineoplastic, antibacterial, activities, and  
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,  
 CC proteins and antibodies to the proteins are useful for the prevention,  
 CC treatment and diagnosis of colon disorders, such as colon cancer. The  
 CC polynucleotides may be used in diagnostics and research, such as for  
 CC chromosome identification, and as hybridisation probes. The proteins  
 CC may also be used to prevent diseases such as neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, wounds, renal disorders, infectious  
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
 CC AAB54007 represent sequences used in the exemplification of the present  
 CC invention.  
 CC  
 XX  
 XX Sequence 259 AA;

Query Match 0.6%; Score 8; DB 21; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEBEQKER 46  
 DB 174 EEBEQKER 181

RESULT 40  
 AAG07235  
 ID AAG07235 standard; Protein; 358 AA.  
 XX  
 AC AAG07235;  
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 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 4311.  
 XX  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 XX Arabidopsis thaliana.

XX EP103405-A2.  
PN  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 29-MAR-1999; 99US-0126264.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0128845.  
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PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
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PR 06-MAY-1999; 99US-0132485.  
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PR 01-JUN-1999; 99US-0137222.  
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XX 18-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;  
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XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

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Qy 145 LKSLRRCG 152  
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KW Herbicidal; plant; agriculture; herbicide.
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OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
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PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB ) BAYER AG.
XX
PI Tiejien K, Weidner M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,

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PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
XX organisms -  
PS Claim 5; SEQ ID NO 2097; 261pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying target proteins  
CC (AB990790-AB994016) for hericidally active compounds, comprising  
CC aligning and comparing nucleic acid or amino acid sequences from plant  
CC with nucleic acid or amino acid sequences from non-plant organisms using  
CC suitable search parameters, where plant sequences having an E-value  
CC greater by a factor of 3 than the E-value of most similar non-plant  
CC sequences are selected. The polypeptides or nucleic acids encoding them  
CC are useful for identifying modulators. The identified modulators are  
CC useful as herbicides.  
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SQ Sequence 358 AA;  
  
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Best Local Similarity 100.0%; Pred. No. 76;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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KW termination sequence.  
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PR 22-OCT-1999; 99US-0160981-  
PR 22-OCT-1999; 99US-0160989-  
PR 22-OCT-1999; 99US-0160989-

PR 25-OCT-1999; 99US-0161404-  
PR 25-OCT-1999; 99US-0161405-  
PR 25-OCT-1999; 99US-0161406-  
PR 26-OCT-1999; 99US-0161359-  
PR 26-OCT-1999; 99US-0161360-  
PR 26-OCT-1999; 99US-0161361-  
PR 26-OCT-1999; 99US-0161920-  
PR 28-OCT-1999; 99US-0161920-  
PR 28-OCT-1999; 99US-0161992-  
PR 28-OCT-1999; 99US-0161993-  
PR 29-OCT-1999; 99US-0162142-  
  
Query Match 0.6%; Score 8; DB 21; Length 373;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 145 LKSRIRGG 152  
Db 95 LKSRIRGG 102  
  
RESULT 44  
AAG07234  
ID AAG07234 standard; Protein; 374 AA.  
XX  
AC AAG07234;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4310.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridization assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000BP-0301439.  
XX  
XX  
PR 25-FEB-1999; 99US-0121825-  
PR 05-MAR-1999; 99US-0123180-  
PR 09-MAR-1999; 99US-0123548-  
PR 23-MAR-1999; 99US-0125788-  
PR 25-MAR-1999; 99US-0126264-  
PR 29-MAR-1999; 99US-0126785-  
PR 01-APR-1999; 99US-0127462-  
PR 06-APR-1999; 99US-0128234-  
PR 08-APR-1999; 99US-0128714-  
PR 16-APR-1999; 99US-0129845-  
PR 19-APR-1999; 99US-0130077-  
PR 21-APR-1999; 99US-0130449-  
PR 23-APR-1999; 99US-0130510-  
PR 28-APR-1999; 99US-0130891-  
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PR 04-MAY-1999; 99US-0132407-  
PR 05-MAY-1999; 99US-0132484-  
PR 06-MAY-1999; 99US-0132485-  
PR 06-MAY-1999; 99US-0132486-  
PR 07-MAY-1999; 99US-0132487-  
PR 11-MAY-1999; 99US-0134256-  
PR 14-MAY-1999; 99US-0134218-  
PR 14-MAY-1999; 99US-0134219-  
PR 14-MAY-1999; 99US-0134221-  
PR 14-MAY-1999; 99US-0134370-  
PR 18-MAY-1999; 99US-0134768-  
PR 19-MAY-1999; 99US-0134941-  
PR 20-MAY-1999; 99US-0135124-  
PR 21-MAY-1999; 99US-0135353-  
PR 21-MAY-1999; 99US-0135353-

PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140951.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142820.  
PR 12-JUL-1999; 99US-0142877.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 11-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 0.6%; Score 8; DB 21; Length 374;  
Best Local Similarity 100.0%; Pred. No. 79;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 LKSLRGG 152  
|||  
DB 96 LKSLRGG 103

RESULT 45  
AAR12352

ID AAR12352 standard; Protein; 428 AA.

AC AAR12352;

DT 14-AUG-1991 (first entry)

DE Toxoplasma gondii P66 antigen.

KM Toxoplasmosis; vaccine; P66.

OS Toxoplasma gondii.

PN EP431541-A.

PD 12-JUN-1991.

PR 04-DEC-1990; 90EP-0123152.

PR 08-DEC-1989; 89DE-3940598.

PA (BEHW) BEHRINGWERKE AG.

PI Knapp S, Ziegelemaier R, Kupper H;

DR WPI; 1991-172854/24.

DR N-PSDB; AAQ11918.

PT New Toxoplasma gondii protein, nucleic acid and derived

PT antibodies - useful as diagnostic reagents, vaccines and for

PS Claim 1; Table 10; 28pp; German.

CC A CDNA fragment encoding P66 was isolated from a T.gondii gene

CC bank. Recombinant protein was produced as part of a fusion protein

CC with beta-galactosidase. The hybrid protein was found to react

CC specifically with IgG antibodies in most of the 21 serum samples

CC tested from humans with acute and chronic T.gondii infection.

CC c.f. P68 and P35 hybrid proteins (see AAR12351 and AAR12353) which

CC reacted with all 21 samples.

CC See also AAQ11909-011917 and AAQ11919.

QY 105 FGAGLTRL 112  
|||  
DB 395 FGAGLTRL 402

RESULT 46  
AAV34752

ID AAV34752 standard; Protein; 441 AA.

AC AAV34752;

XX 13-SEP-1999 (first entry)

DT Chlamydia pneumoniae transmembrane protein sequence.

DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

XX vaccine; neutralising epitope.

OS Chlamydia pneumoniae.

PN MO927105-A2.

PD 03-JUN-1999.

PR 20-NOV-1998; 98MO-IB01890.

PR 04-NOV-1998; 98US-0107078.

PR 21-NOV-1997; 97PR-0014673.

PA (GENT) GENSET.

PI Griffiths R;

DR WPI; 1999-357842/30.

PT Genome sequence of Chlamydia pneumoniae

PS Page 739-740; Disclosure; 1912pp; English.

CC AAY34584-Y35879 represent the proteins encoded by all the open reading

CC frames in the complete genome (see AAY31990) of Chlamydia pneumoniae.

CC C. pneumoniae causes respiratory disease such as pneumonia and

CC bronchitis and is thought to be a contributing factor in heart

CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema

CC nodosum or pharyngitis. The polypeptides encoded by the open reading

CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in

CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae

CC nucleotide sequences can also be used as immunogenic compositions,

CC especially where the vector directs the expression of a neutralising

CC epitope of C. pneumoniae.

QY 102 LILFGAGL 109  
|||  
DB 135 LILFGAGL 142

RESULT 47  
AAW19745

ID AAW19745 standard; Protein; 496 AA.

AC AAW19745;

DT 16-SEP-1997 (first entry)

DE Mouse inhibitor of apoptosis protein homologue MIHA.

KM Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;

XX degenerative disease; infectious disease; autoimmune disease;

XX cancer; therapy; diagnosis.

OS Mus musculus.

PN Key

FT Region

FT Location/Qualifiers

FT 26..93

FT /label= BIR

FT 163..230



FT	Region	/label= BIR 264..330
FT	Region	/label= BIR
FT	Region	448..485
FT		/label= RING_finger
PN	MO9723501-A1.	
XX		
XX	03-JUL-1997.	
XX		
PF	20-DEC-1996;	96WO-AU00827.
XX		
PR	22-DEC-1995;	95AU-0007275.
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.	
XX		
PI	Vaux DL;	
XX		
DR	WPI: 1997-350966/32.	
DR	N-PSDB; AAT72710.	
XX		
PT	Isolated protein homologues of viral inhibitors of apoptosis - used	
PT	to modulate apoptosis for treatment of degenerative, infectious or	
PT	autoimmune diseases and cancer	
XX		
ES	Claim 7; Page 44-47; 136pp; English.	
XX		
CC	Mammalian IAP homologue A (MHA) (AAW19745) is a murine homologue of	
CC	baculovirus inhibitor of apoptosis protein (IAP) . Its amino acid	
CC	sequence was deduced from a cDNA clone (see also AAT72710) isolated	
CC	from a mouse liver cDNA library on the basis of homology to Oryzias	
CC	pseudotubula polydrosis virus IAP BIR and RING finger amino acid	
CC	motifs (see also AAW19744) . IAP homologues (see also AAW19746-52) and	
CC	their derivatives and chemical analogues can be used in methods for	
CC	modulating apoptosis in animal cells, specifically for treatment,	
CC	by inhibition, of degenerative and infectious disease or, by	
CC	promotion, of cancer and autoimmune disease.	
XX		
SQ	Sequence 496 AA;	
	Query Match 0.6%; Score 8; DB 18; Length 496;	
	Best Local Similarity 100.0%; Pred. No. 1e+02;	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	193 DTVOCFSC 200	
	59 DTVOCFSC 66	
DB		
	RESULT 48	
	AAW19584	
ID	AAW19584 standard; Protein; 496 AA.	
XX		
AC	AAW19584;	
XX		
DT	02-SEP-1997 (first entry)	
XX		
DE	Mouse apoptosis inhibitor M-XIAP.	
XX		
KM	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;	
KM	M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;	
KW	ischemia; myocardial infarction; stroke;	
KW	reperfusion injury; toxin-induced liver disease; gene therapy;	
diagnosis.		
XX		
OS	Mus sp.	
XX		
Key	Location/Qualifiers	
FT	26..93	
FT	/label= BIR-1	
FT	163..230	
FT	/label= BIR-2	
FT	264..329	
FT	Domain	

FT	FT	Domain	/label= BIR-3
FT	FT		438..483
XX	XX		/label= Ring_zinc_finger
PN	PN	WO9706255-A2.	
XX	XX		
PD	PD	20-FEB-1997.	
XX	XX		
FP	FP	05-AUG-1996;	96WO-IB01022.
XX	XX		
PR	PR	22-DEC-1995;	95US-0576956.
XX	XX	04-AUG-1995;	95US-0511485.
PA	PA	(UYOT-) UNIV OTTAWA.	
XX	XX		
P1	P1	Baird S, Korneluk RG, Liston P, Mackenzie AE;	
XX	XX		
DR	DR	WPI: 1997-154262/14.	
DR	DR	N-PSDB; AAT70839.	
XX	XX		
FT	FT	Nucleic acid encoding an inhibitor of apoptosis polypeptide - used	
FT	FT	to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection	
PT	PT	of susceptibility to apoptotic disease	
XX	XX		
PS	PS	Claim 27; Page 79-80; 21pp; English.	
XX	XX		
CC	CC	Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and	
CC	CC	M-HIAP-2 (AAW19581-86) are a new class of mammalian proteins that	
CC	CC	are inhibitors of apoptosis (IAP) and which are characterised by	
CC	CC	the presence of a ring zinc finger domain (see also AAW19587) and at	
CC	CC	least one BIR (baculovirus IAP repeat) domain (see also AAW19588).	
CC	CC	The M-XIAP amino acid sequence was deduced from the m-xiap gene	
CC	CC	(AAT70839) isolated from a mouse embryo cDNA library. The IAP	
CC	CC	olypeptides can be expressed in host cells (in vitro or in	
CC	CC	vivo) and used in methods for treating diseases and disorders	
CC	CC	involving apoptosis, esp. in a human diagnosed as HIV-positive or	
CC	CC	as having AIDS, a neurodegenerative disease, a myelodysplastic	
CC	CC	syndrome or an ischemic injury, selected from myocardial infarction,	
CC	CC	stroke, reperfusion injury, or a toxin-induced liver disease.	
XX	XX		
SQ	SQ	Sequence 496 AA;	
QY	Query Match	0.6%; Score 8; DB 18; Length 496;	
	Best Local Similarity	100.0%; Pred. No. 1e+02;	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	193 DTVOCFSC 200		
	59 DTVOCFSC 66		
RESULT 49			
AAW69297			
ID	AAW69297 standard; Protein; 496 AA.		
XX	AAW69297;		
XX			
DT	13-NOV-1998 (first entry)		
XX			
DE	Murine XIAP protein.		
XX			
KW	Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;		
KM	proliferative disease; IAP; therapy; cancer; mouse; XIAP protein.		
XX			
OS	Mus sp.		
XX			
PN	WO9835693-A2.		
XX			
PD	20-AUG-1998.		
XX			
PP	13-FEB-1998; 98WO-IB00781.		
XX			
PR	13-FEB-1997; 97US-0800929.		

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XX (UYOT-) UNIV OTTAWA.
PA Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX WPI; 1998-467164/40.
DR N-PSDB; AAV55041.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PS p53 mutations
PS Disclosure; Fig 4; 147pp; English.
XX
XX This sequence is the murine XIAP protein, which is a inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX
SQ Sequence 496 AA;
XX
XX Query Match 0.6%; Score 8; DB 19; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 193 DTVOCFSC 200
XX |||||
Db 59 DTVOCFSC 66
XX
XX RESULT 50
XX ABG65666
XX ID ABG65666 standard; Protein; 496 AA.
XX
XX AC ABG65666;
XX
XX DT 26-AUG-2002 (first entry)
XX
XX DE Mouse inhibitor of apoptosis, XIAP.
XX
XX KW Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
XX cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
XX pancreatic cancer; embryonic development; viral pathogenesis;
XX autoimmune disorder; neurodegenerative disease; multiple sclerosis;
XX lupus erythematosus; herpes virus infection; pox virus infection;
XX adenovirus infection; proliferative disease.
XX
XX Mus sp.
XX
XX WO200226968-A2.
XX
XX PD 04-APR-2002.
XX
XX PF 27-SEP-2001; 2001WO-CA01379.
XX
XX PR 28-SEP-2000; 2000US-0672717.
XX
XX (UYOT-) UNIV OTTAWA.
XX PA (AEGE-) AEGERA THERAPEUTICS INC.
XX

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PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
DR N-PSDB; ABK93872.
XX
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases -
XX
XX Example 12; Fig 4; 135pp; English.
XX
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (i) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
CC protein sequence.
XX
SQ Sequence 496 AA;
XX
XX Query Match 0.6%; Score 8; DB 23; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 193 DTVOCFSC 200
XX |||||
Db 59 DTVOCFSC 66
XX
XX RESULT 51
XX ABP72157
XX ID ABP72157 standard; Protein; 496 AA.
XX
XX AC ABP72157;
XX
XX DT 22-APR-2003 (first entry)
XX
XX DE Mouse inhibitor of apoptosis protein MIAP3.
XX
XX KW Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukemia;
XX lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic;
XX gene therapy.
XX
XX Mus sp.
XX
XX WO2003004606-A2.
XX
XX PD 16-JAN-2003.
XX
XX PF 03-JUL-2002; 2002WO-US21002.
XX
XX PR 03-JUL-2001; 2001US-0898158.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX PI Troy CM, Shelanski ML;
XX
XX WPI; 2003-210351/20.
XX DR N-PSDB; ABZ58102.
XX
XX New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for

```

PT treating cancer, neurodegenerative disorder or cardiomyopathy -  
 XX  
 PS Disclosure; Fig 15A; 124pp; English.  
 XX  
 CC The present sequence is the protein sequence of murine inhibitor of  
 CC apoptosis protein MIAP3. The invention provides a nucleic acid,  
 CC such as an antisense oligonucleotide, which specifically hybridises  
 CC to a nucleic acid encoding an inhibitor of apoptosis protein,  
 CC especially MIAP1, MIAP2, MIAP3, CIAP1, CIAP2 and XIAP. A claimed  
 CC method for inducing a cell's death comprises contacting the cell  
 CC with the nucleic acid under conditions permitting the nucleic acid  
 CC to enter the cell, especially the use of a vector, liposome, or a  
 CC mechanical or electrical means. The method is used to treat acute  
 CC lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer,  
 CC breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's  
 CC disease, malignant melanoma, neuroblastoma, renal cell carcinoma  
 CC and squamous cell carcinoma (all claimed).  
 XX  
 SQ Sequence 496 AA;  
 Query Match 0.6%; Score 8; DB 24; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;  
 Matches 8; Conservative 0; Indels 0;  
 QY 193 DTVCQCFSC 200  
 |||||  
 59 DTVCQCFSC 66  
 DB  
 RESULT 52  
 ID ABP41530 standard; Protein; 506 AA.  
 XX  
 AC ABP41530;  
 XX  
 DT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HFIAS44, SEQ ID NO:2662.  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive; chromosome 14.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WPI; 2002-147878/19.  
 XX  
 DR N-PSDB; ABO54607.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX  
 PS Claim 11; SEQ ID NO 2662; 2922pp; English.

XX  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
 CC encompasses polypeptides 908 identical and polynucleotides 958 identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 506 AA;  
 Query Match 0.6%; Score 8; DB 23; Length 506;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Gaps 0;  
 Matches 8; Conservative 0; Indels 0;  
 QY 39 EEEBOKER 46  
 |||||  
 483 EEEBOKER 490  
 DB

RESULT 53  
 ID ABG09940 standard; Protein; 519 AA.  
 XX  
 AC ABG09940;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #9931.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 XX  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSR-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 XX  
 DR N-PSDB; AAS74127.  
 XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT blood/urivervily -

PS Claim 20; SEQ ID No 40299; 103pp; English  
XY

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probe, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABC00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).

**5Q Sequence 519 AA;**

```

Query Match      0.64; Score 8; DB 22; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 0; Gaps 0

```

```

QY      39 EEEEEQKER 46
         |||||
Db      434 EEEEEQKER 441

```

RESULT 54  
ABB61920  
ID ABB61920 standard; Protein; 521 AA  
XX

ABB61920;

DT 26-MAR-2002 (first entry)

*Drosophila melanogaster* polypeptide SEQ ID NO 12552

pharmaceutical.

*Drosophila melanogaster*

WQ200171042-A2

27-SEP-2001

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.  
11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

Venter JC, Adams M, Ll PWD, Myers EW;

WPI; 2001-656860/75

### New isolated nucleic

... PROBABILITY

New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell

PT interactions -  
XX  
PS Disclosure; SEQ ID NO 12552; 21pp + Sequence Listing; English  
XX

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16175-AB170511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (AB57737-AB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIP0 at [ftp.wipo.int/publ/published\\_pcc\\_sequences](http://wipo.int/publ/published_pcc_sequences).

**SQ Sequence 521 AA**

```

Query Match      0.6%; Score 8; DB 22; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	28	GLDAVQLA	35
Db	233	GLDAVQLA	240

RESULT 55	
AAR71976	
ID AAR71976	standard; Protein; 523 AA
XY	

AC AAR71976;  
XY

DT	25-MAR-2003	(updated)
DT	15-MAY-1995	(first entry)
xy		

DE Pertu8818 A  
xy

Bordetella pertussis

XX  
XX

XXXXXXXXXXXX

[illegible]

21

XX 15-MAR-1993

(AMCY ) AMERICAN CYANAMID CO

PI Baker SM, Deich RA;

DR WPI; 1994-304463/38.

2000

- is located 3' of the ptx c  
secretion of holotoxin for

Example 1: Fig 1: 26bp: Enc1

AAQ74445 is a DNA sequence 1

Example 1; Fig 1; 26pp; English.

AA074445 is a DNA sequence located 3' of the *Bordetella pertussis* (Bp) ptx operon, it encodes pertussis A (AA071976) and B (AA072100); these gene products are involved in the expression or secretion of Bp holotoxin. AA074445 was used in the construction of a plasmid, which enabled the expression, assembly and secretion of Bp holotoxin to be regulated in a homologous or heterologous host. These hosts could then be used for the production of large quantities of holotoxin, for use as a vaccine.

(updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 523 AA;  
 Query Match 0.6%; Score 8; DB 15; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 GSGKTVLL 480  
 DB 459 GSGKTVLL 466

RESULT 56  
 ABB67078  
 ID ABB67078 standard; Protein; 538 AA.  
 AC ABB67078;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 28026.  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 XX Drosophila melanogaster.  
 OS  
 XX WO200171042-A2.  
 PN 27-SEP-2001.  
 PD 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 XX 11-JUL-2000; 2000US-0614150.  
 PR (PEXE ) PE CORP NY.  
 PA Venter JC, Adams M, Li PMD, Myers EM;  
 PI N-PSDB; ABL1181.  
 DR WPI: 2001-656860/75.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions  
 PS Disclosure; SEQ ID NO 28026; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB16175), expressed DNA  
 CC sequences (AB16176-AB16175) and the encoded proteins  
 CC (AB16176-AB16175).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 538 AA;

Query Match 0.6%; Score 8; DB 22; Length 538;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 SAVGAAL 299  
 DB 340 SAVGAAL 347

RESULT 57  
 AAM8788

ID AAM8788 standard; Protein; 567 AA.  
 XX  
 AC AAM8788;  
 XX  
 DT 01-MAR-1999 (first entry)  
 DE Polypeptide fragment encoded by gene 36.  
 XX  
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9854963-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 04-JUN-1998; 98WO-US11422.  
 XX  
 PR 18-DEC-1997; 97US-0070923.  
 PR 06-JUN-1997; 97US-0048877.  
 PR 06-JUN-1997; 97US-0048881.  
 PR 06-JUN-1997; 97US-0048884.  
 PR 06-JUN-1997; 97US-0048893.  
 PR 06-JUN-1997; 97US-0048896.  
 PR 06-JUN-1997; 97US-0048899.  
 PR 06-JUN-1997; 97US-0048915.  
 PR 06-JUN-1997; 97US-0048949.  
 PR 06-JUN-1997; 97US-0048964.  
 PR 06-JUN-1997; 97US-0048972.  
 PR 06-JUN-1997; 97US-0049020.  
 PR 06-JUN-1997; 97US-0049375.  
 PR 06-JUN-1997; 97US-0057628.  
 PR 05-SEP-1997; 97US-0057635.  
 PR 05-SEP-1997; 97US-0057644.  
 PR 05-SEP-1997; 97US-0057647.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057661.  
 PR 05-SEP-1997; 97US-0057667.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 05-SEP-1997; 97US-0057764.  
 PR 05-SEP-1997; 97US-0057770.  
 PR 05-SEP-1997; 97US-0057775.  
 PR 05-SEP-1997; 97US-0057778.  
 PR 06-JUN-1997; 97US-0048875.  
 PR 06-JUN-1997; 97US-0048878.  
 PR 06-JUN-1997; 97US-0048882.  
 PR 06-JUN-1997; 97US-0048885.  
 PR 06-JUN-1997; 97US-0048894.  
 PR 06-JUN-1997; 97US-0048897.  
 PR 06-JUN-1997; 97US-0048900.  
 PR 06-JUN-1997; 97US-0048916.  
 PR 06-JUN-1997; 97US-0048962.  
 PR 06-JUN-1997; 97US-0048970.  
 PR 06-JUN-1997; 97US-0048974.  
 PR 06-JUN-1997; 97US-0049373.  
 PR 05-SEP-1997; 97US-0057584.  
 PR 05-SEP-1997; 97US-0057629.  
 PR 05-SEP-1997; 97US-0057642.  
 PR 05-SEP-1997; 97US-0057645.  
 PR 05-SEP-1997; 97US-0057648.  
 PR 05-SEP-1997; 97US-0057651.  
 PR 05-SEP-1997; 97US-0057662.  
 PR 05-SEP-1997; 97US-0057668.  
 PR 05-SEP-1997; 97US-0057762.  
 PR 05-SEP-1997; 97US-0057765.  
 PR 05-SEP-1997; 97US-0057771.

PR 05-SEP-1997; 97US-0057776.  
 PR 06-JUN-1997; 97US-0048876.  
 PR 06-JUN-1997; 97US-0048880.  
 PR 06-JUN-1997; 97US-0048883.  
 PR 06-JUN-1997; 97US-0048892.  
 PR 06-JUN-1997; 97US-0048895.  
 PR 06-JUN-1997; 97US-0048898.  
 PR 06-JUN-1997; 97US-0048901.  
 PR 06-JUN-1997; 97US-0048917.  
 PR 06-JUN-1997; 97US-0048963.  
 PR 06-JUN-1997; 97US-0048971.  
 PR 06-JUN-1997; 97US-0049019.  
 PR 05-SEP-1997; 97US-0049374.  
 PR 05-SEP-1997; 97US-0057627.  
 PR 05-SEP-1997; 97US-0057634.  
 PR 05-SEP-1997; 97US-0057643.  
 PR 05-SEP-1997; 97US-0057646.  
 PR 05-SEP-1997; 97US-0057649.  
 PR 05-SEP-1997; 97US-0057654.  
 PR 05-SEP-1997; 97US-0057660.  
 PR 05-SEP-1997; 97US-0057763.  
 PR 05-SEP-1997; 97US-0057769.  
 PR 05-SEP-1997; 97US-0057774.  
 PR 05-SEP-1997; 97US-0057777.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;  
 PI Fan P, Ferrie AM, Fischer CL, Florence C;  
 PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;  
 PI Li Y, Moore PA, Ni U, Olsen HS, Rosen CA, Ruben SM;  
 PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;  
 XX MPI; 1999-059865/05.  
 DR N-PSDB; AAV84446.  
 XX  
 PT New isolated human genes and the secreted polypeptides they encode -  
 PT useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 XX  
 PS Disclosure; Page 30; 772pp; English.  
 XX  
 CC The invention relates to nucleic acid sequences (AAV84411 to AAV84633)  
 CC encoding human secreted proteins (AAV8534 to AAV8756). The secreted  
 CC protein gene sequences are deposited with the ATCC under deposit numbers  
 CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,  
 CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host  
 CC cells comprising recombinant vectors containing the nucleic acid  
 CC sequences are used for the recombinant production of the secreted  
 CC proteins. The polynucleotide and amino acid sequences are useful for are  
 CC useful for preventing, treating or ameliorating medical conditions e.g.  
 CC by protein or gene therapy. Pathological conditions can be also  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new polynucleotides.  
 CC Specific uses are described for each of the polynucleotides, based on  
 CC products for the diagnosis or treatment of cancer, neurodegenerative  
 CC disorders, developmental abnormalities and foetal deficiencies, blood  
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune  
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,  
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,  
 CC retinoblasts, prostate diseases, obesity, disorders involving osteoclasts  
 CC such as osteoporosis, arthritis or malignancies, diseases of testes,  
 CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The  
 CC polypeptides are also useful for identifying their binding partners.  
 CC The present sequence represents a polypeptide fragment encoded by a  
 CC gene of the invention (see descriptor line for gene number).  
 XX  
 SO Sequence 567 AA;  
 Query Match 0.64; Score 8; DB 20; Length 567;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 39 EREBOOKER 46  
 Db 483 EREBOOKER 490  
 RESULT 58  
 ABB50625  
 ID ABB50625 standard; Protein; 567 AA.  
 XX  
 AC ABB50625;  
 XX  
 DT 07-FEB-2002 (first entry)  
 XX  
 DE Human secreted protein encoded by gene 36 SEQ ID NO:573.  
 XX  
 KW Human; secreted protein; immunomodulatory; antileukemic; anti-HIV;  
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 KW cytototoxic; cardiant; anti-angiogenic; ophthalmological;  
 KW neuroprotective; nocotropic; anticonvulsant; antialzheimer's; vulnery;  
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;  
 KW Gaucher's disease; cardiovascular disease; Schifter syndrome; chemotaxis;  
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiotensin disorder;  
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease; chromosome 14.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200162891-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 21-FEB-2001; 2001WO-US05614.  
 XX  
 PR 24-FEB-2000; 2000US-184836P.  
 PR 29-MAR-2000; 2000US-193170P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ni U, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;  
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;  
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;  
 PI Peng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;  
 PI Zeng Z, Greene JM;  
 XX  
 DR MPI; 2001-625724/72.  
 XX  
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX  
 PS Disclosure; Page 84-85; 1533pp; English.  
 XX  
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted  
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Example of these activities include: immunomodulatory; antileukemic;  
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 CC anti-HIV; cytototoxic; cardiant; anti-angiogenic; ophthalmological;  
 CC neuroprotective; nocotropic; anticonvulsant; antialzheimer's; vascular;  
 CC antiparkinsonian; antidiabetic; and vulnery. (I) and (II) can be used  
 CC in gene therapy and vaccine production. (I) and (II) can be used in the  
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 CC Gaucher's disease), cardiovascular diseases (e.g. Schifter syndrome,  
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiotensin  
 CC disorders (e.g. corneal graft neovascularisation and diabetic  
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,

CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 CC ABA83193 and ABA850300 represent sequences used in the exemplification of  
 CC the present invention.

XX Sequence 567 AA;

Query Match 0.6%; Score 8; DB 22; Length 567;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEBQKER 46  
 DB 483 EEEBQKER 490

RESULT 59  
 AAY85658  
 ID AAY85658 standard; Protein; 568 AA.

XX AAY85658;  
 AC  
 XX 12-FEB-2001 (first entry)  
 DT  
 XX Human Acinus S protein sequence.  
 DE

XX Chromatin aggregation induction; human; Acinus; AIDS; herpes; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; cardiac infarction;  
 KW brain infarction; adenovirus infection; viral hepatitis.

XX Homo sapiens.  
 OS  
 XX WO200061743-A1.  
 PN  
 XX 19-OCT-2000.  
 PD

XX 07-APR-2000; 2000WO-JP02254.  
 PF

XX 09-APR-1999; 99JP-0103317.  
 PR  
 XX (SHIO) SHIONOGI & CO LTD.  
 PA

XX Sahara S, Eguchi Y, Tsujimoto Y;  
 PI  
 XX MPI: 2000-665130/64.  
 DR  
 XX N-PSDB; AAC61197.  
 DR

XX A novel polypeptide which induces chromatin aggregation but is not  
 PT involved in DNA fragmentation used for the regulation of apoptosis and  
 PT screening of potential apoptosis inhibitors -  
 XX

XX Disclosure; Page 91-95; 99pp; Japanese.

XX This invention relates to a polypeptide which induces chromatin  
 CC aggregation. The polypeptide is a fragment of the human Acinus protein.  
 CC included in the invention is a nucleotide sequence encoding the  
 CC polypeptide, antisense oligonucleotides, antibodies recognizing the  
 CC polypeptide sequence, and apoptosis regulating agents containing the  
 CC oligonucleotides. Also included in the invention is a method for  
 CC screening compounds for their activity as chromatin aggregation  
 CC inhibitors, regulators or promoters. The polypeptide induces chromatin  
 CC aggregation within the cell nucleus without inducing DNA fragmentation.  
 CC The polypeptide can be used in the investigation and treatment of  
 CC diseases in which apoptosis is implicated, including AIDS, Alzheimer's  
 CC disease, Parkinson's disease, cardiac or brain infarction, herpes or  
 CC adenovirus infection, diabetes and viral hepatitis. The present sequence  
 CC represents the human Acinus protein.

XX Sequence 568 AA;

Query Match 0.6%; Score 8; DB 21; Length 568;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 EEEBQKER 46  
 DB 483 EEEBQKER 490

RESULT 60  
 ABB71239  
 ID ABB71239 standard; Protein; 575 AA.

XX ABB71239;  
 AC  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Drosophila melanogaster polypeptide SEQ ID NO 40509.  
 DE

XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 KW

XX Drosophila melanogaster.  
 OS  
 XX WO200171042-A2.  
 PN  
 XX 27-SEP-2001.  
 PD

XX 23-MAR-2001; 2001WO-US09231.  
 PF

XX 23-MAR-2000; 2000US-191637P.  
 PR  
 XX 11-JUL-2000; 2000US-0614150.  
 PR

XX (PEKE) PE CORP NY.  
 PA  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 PI  
 XX MPI: 2001-656860/75.  
 DR  
 XX N-PSDB; ABL15342.  
 DR

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX

XX Disclosure; SEQ ID NO 40509; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 575 AA;

Query Match 0.6%; Score 8; DB 22; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 SAVGVAAL 299  
 DB 377 SAVGVAAL 384

RESULT 61  
 AAY85659  
 ID AAY85659 standard; Protein; 583 AA.

XX AAY85659;  
 AC  
 XX

DT 12-FEB-2001 (first entry)  
 XX Human Actinus 5' protein sequence.  
 DE  
 XX Chromatin aggregation induction; human; Actinus; AIDS; herpes; diabetes;  
 KM Alzheimer's disease; Parkinson's disease; cardiac infarction;  
 KM brain infarction; adenovirus infection; viral hepatitis.  
 XX Homo sapiens.  
 OS  
 XX WO200061743-A1.  
 PN  
 XX 19-OCT-2000.  
 PD  
 XX 07-APR-2000; 2000WO-JP02254.  
 PF  
 XX 09-APR-1999; 99JP-0103317.  
 PR  
 XX (SHIO) SHIONOGI & CO LTD.  
 PA  
 XX Sahara S, Eguchi Y, Tsujimoto Y;  
 PI  
 XX WPI; 2000-665130/64.  
 DR  
 XX N-PSDB; AAC61198.  
 PT  
 XX A novel polypeptide which induces chromatin aggregation but is not  
 PT involved in DNA fragmentation used for the regulation of apoptosis and  
 PT screening of potential apoptosis inhibitors  
 PS Disclosure; Page 67-70; 99pp; Japanese.  
 XX  
 XX This invention relates to a polypeptide which induces chromatin  
 CC aggregation. The polypeptide is a fragment of the human Actinus protein.  
 CC included in the invention is a nucleotide sequence encoding the  
 CC polypeptide, antisense oligonucleotides, antibodies recognizing the  
 CC polypeptide sequence, and apoptosis regulating agents containing the  
 CC polypeptide, nucleotide sequence, and sense or antisense  
 CC oligonucleotides. Also included in the invention is a method for  
 CC screening compounds for their activity as chromatin aggregation  
 CC inhibitors, regulators or promoters. The polypeptide induces chromatin  
 CC aggregation within the cell nucleus without inducing DNA fragmentation.  
 CC The polypeptide can be used in the investigation and treatment of  
 CC diseases in which apoptosis is implicated, including AIDS, Alzheimer's  
 CC disease, Parkinson's disease, cardiac or brain infarction, herpes or  
 CC adenovirus infection, diabetes and viral hepatitis. The present sequence  
 CC represents the human Actinus protein.  
 CC  
 SO Sequence 583 AA;  
 Query Match 0.6%; Score 8; DB 21; Length 583;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 39 EEEEXKX 46  
 DB 498 EEEEXKX 505  
 RESULT 62  
 AAG09939 standard; Protein; 614 AA.  
 ID AAG09939;  
 AC AAG09939;  
 DT 13-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #9930.  
 XX  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 OS  
 XX Homo sapiens.  
 XX

PN WO200175067-A2.  
 XX  
 XX 11-OCT-2001.  
 PD  
 XX 30-MAR-2001; 2001WO-US08631.  
 PF  
 XX 31-MAR-2000; 2000US-0540217.  
 PR  
 XX 23-AUG-2000; 2000US-0649167.  
 OS  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Drenanac RT, Liu C, Tang YT;  
 PI  
 XX WPI; 2001-639362/73.  
 DR  
 XX N-PSDB; AAG74126.  
 PT  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 PS Claim 20; SEQ ID No 40298; 103pp; English.  
 XX  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAG00010-AAG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SO Sequence 614 AA;  
 Query Match 0.6%; Score 8; DB 22; Length 614;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 39 EEEEXKX 46  
 DB 529 EEEEXKX 536  
 RESULT 63  
 AAY57754  
 ID AAY57754 standard; Protein; 654 AA.  
 XX  
 XX AAY57754;  
 AC  
 DT 16-MAR-2000 (first entry)  
 DE CKS-P66-CKS fusion protein protein sequence.  
 XX  
 XX Toxoplasmosis; antigen; P29; vaccine; coccidiostatic; antibody;  
 KM diagnosis; infection; identification.  
 OS  
 XX Toxoplasma gondii.  
 OS  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH



```

FT MISC-difference 251
XX /note="unspecified"
XX
XX WO961906-A2.
XX
XX 02-DEC-1999.
XX
XX 27-MAY-1999; 99WO-US11720.
XX
XX 28-MAY-1998; 98US-0086503.
XX
XX 30-APR-1999; 99US-0303064.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX MAINE CT, Hunt JC, Brojanac S, Shou MJ, Chovan LE, Tyner JD;
PI Howard LV, Parmley SF, Remington JS, Araujo F, Suzuki Y, Li S;
XX
XX WPI; 2000-072663/06.
XX
XX N-PSDB; AA256330.
XX
XX Composition useful for diagnosing toxoplasmosis -
XX
XX Example 11; Fig 13; 169pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX combination of Toxoplasma gondii antigens (Ag) such as novel P29, along
XX with P35 and P30/P66 (I) is useful in detecting T. gondii specific
XX (immunoglobulin) IgM/IgG antibodies, which is useful in diagnosing
XX toxoplasmosis. P35 antigen is useful in distinguishing between acute
XX and chronic toxoplasmosis. (I) is also useful as vaccines. In combination
XX with other known antigens, P29 accurately detects the presence of IgG or
XX IgM, in the test sample, hence eliminates the problem of false negative
XX or false positive tests. T. gondii P35 IgG immunoassay detects only the
XX T. gondii IgG Abs present in acute infection and does not detect IgG
XX antibodies in chronic infection, which facilitates an accurate diagnosis
XX of the infection stage, which is useful for the clinical management. The
XX present sequence represents a fusion protein, from an example in the
XX present invention.
XX
XX Sequence 654 AA;
XX
XX Query Match 0.6%; Score 8; DB 21; Length 654;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 105 FGAGLTRL 112
XX |||||
XX 529 FGAGLTRL 536
XX
XX RESULT 64
XX ABB71989
XX ID ABB71989 standard; Protein; 679 AA.
XX
XX AC ABB71989;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 42759.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.

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XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EM;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL16092.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 42759; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABBS7737-ABR22072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 679 AA;
XX
XX Query Match 0.6%; Score 8; DB 22; Length 679;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 348 MKSSAEVT 355
XX |||||
XX Db 297 MKSSAEVT 304
XX
XX RESULT 65
XX AAG79222
XX ID AAG79222 standard; Protein; 845 AA.
XX
XX AC AAG79222;
XX
XX 03-JAN-2002 (first entry)
XX
XX Amino acid sequence of an oxoprolinase-like enzyme polypeptide.
XX
XX Human; oxoprolinase-like enzyme; OP-like enzyme; cancer; chemotherapy;
XX radiation therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT MISC-difference 217
XX FT /note="Met encoded by TC"
XX
XX PN WO200173056-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001WO-EP03427.
XX
XX 27-MAR-2000; 2000US-192364P.
XX
XX (PARB ) BAYER AG.
XX
XX Ramakrishnan S;
XX
XX WPI; 2001-616515/71.
XX
XX N-PSDB; AA165824.
XX
XX New polynucleotide encoding a human oxoprolinase-like enzyme,
XX regulation of which is used for enhancing chemotherapy or radiotherapy

```

PT of cancer cells and to protect normal cells during treatment -  
 XX  
 SS Example 1; Fig 4; 71pp; English.

CC The present sequence represents a human oxoprolinase-like (OP-like)  
 CC enzyme. The OP-like polynucleotide is used to produce an OP-like enzyme  
 CC polypeptide, and is also used in a hybridization assay to detect  
 CC similar polynucleotides. The OP-like polynucleotide or polypeptide  
 CC are used to screen for compounds that decrease activity of an OP-like  
 CC polypeptide, or screen for agents that regulate activity of an OP-like  
 CC enzyme. An expression vector or a reagent that modulates OP-like enzyme  
 CC activity is useful to treat a disease, particularly cancer. The  
 CC treatment is used to enhance the effects of chemotherapy or radiation  
 CC therapy of cancer cells and at the same time to protect normal cells  
 CC from the toxic effects of such treatment.

SO Sequence 845 AA;

Query Match 0.6%; Score 8; DB 22; Length 845;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 456 PEVFGNIN 463  
 |||||  
 DB 618 PEVFGNIN 625

RESULT 66  
 ABG66688  
 ID ABG66688 standard; Protein; 848 AA.

XX ABG66688;  
 DT 30-AUG-2002 (first entry)

XX Human novel polypeptide #23.

XX Human; inflammatory condition; shock; sepsis; immune response;  
 KW cancer; wound healing; central nervous system disease; haematopoiesis;  
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;  
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;  
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;  
 KW bone degenerative disorder; periodontal disease; reperfusion injury;  
 KW lung fibrosis; liver fibrosis; autoimmune disease; bacterial infection;  
 KW allergic condition; thrombolysis; thrombosis; coagulation disorder;  
 KW fungal infection;

OS Homo sapiens.

PN WO200244340-A2.

PD 06-JUN-2002.

PF 30-NOV-2001; 2001WO-US47004.

PR 30-NOV-2000; 2000US-0028952.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;  
 PI Yamazaki V, Ujwal ML, Drmanac RT;

DR N-PSDB; ABK94912.

XX WPI; 2002-508509/54.

PT Novel nucleic acids and polypeptides for diagnosis, treatment of  
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell  
 PT disorders, cancer and promoting wound healing -

PS Claim 10; Page 588-589; 672pp; English.

CC The invention relates to human novel polynucleotides and associated  
 CC polypeptides. The polynucleotides and polypeptides are useful for

CC treating inflammatory conditions such as arthritis, nephritis, Crohn's  
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses  
 CC and cancer and for promoting wound healing. The sequences are used to  
 CC induce the proliferation of neural cells and regeneration of nerve and  
 CC brain tissue, and are useful for the treatment of central and peripheral  
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral  
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid  
 CC cell disorders and platelet disorders such as thrombocytopenia,  
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of  
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal  
 CC disease. The sequences of the invention are also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, immune deficiencies and disorders  
 CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia  
 CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis  
 CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human  
 CC novel polypeptides of the invention.

SO Sequence 848 AA;

Query Match 0.6%; Score 8; DB 23; Length 848;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 EEEARLAS 165  
 |||||  
 DB 772 EEEARLAS 779

RESULT 67  
 ABG66687  
 ID ABG66687 standard; Protein; 906 AA.

XX ABG66687;

DT 30-AUG-2002 (first entry)

XX Human novel polypeptide #22.

XX Human; inflammatory condition; shock; sepsis; immune response;  
 KW cancer; wound healing; central nervous system disease; haematopoiesis;  
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;  
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;  
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;  
 KW bone degenerative disorder; periodontal disease; reperfusion injury;  
 KW lung fibrosis; liver fibrosis; autoimmune disease; bacterial infection;  
 KW allergic condition; thrombolysis; thrombosis; coagulation disorder;  
 KW fungal infection.

OS Homo sapiens.

PN WO200244340-A2.

PD 06-JUN-2002.

PF 30-NOV-2001; 2001WO-US47004.

PR 30-NOV-2000; 2000US-0028952.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;  
 PI Yamazaki V, Ujwal ML, Drmanac RT;

DR N-PSDB; ABK94911.

XX WPI; 2002-508509/54.

PT Novel nucleic acids and polypeptides for diagnosis, treatment of  
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell

PT disorders, cancer and promoting wound healing -  
 XX  
 PS Claim 10; Page 586-587; 672pp; English.  
 XX  
 CC The invention relates to human novel polynucleotides and associated  
 CC polypeptides. The polynucleotides and polypeptides are useful for  
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's  
 CC disease, ischemia-reperfusion injury, shock, sepsis, immune responses  
 CC and cancer and for promoting wound healing. The sequences are used to  
 CC induce the proliferation of neural cells and regeneration of nerve and  
 CC brain tissue, and are useful for the treatment of central and peripheral  
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,  
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral  
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid  
 CC cell disorders and platelet disorders such as thrombocytopenia,  
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of  
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal  
 CC disease. The sequences of the invention are also useful for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, immune deficiencies and disorders  
 CC including severe combined immunodeficiency (SCID), bacterial or fungal  
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia  
 CC gravis, allergic conditions such as asthma, thrombolytic or thrombosis  
 CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human  
 CC novel polypeptides of the invention.  
 CC  
 SQ Sequence 906 AA;  
 XX  
 XX  
 Query Match 0.6%; Score 8; DB 23; Length 906;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 158 EEEARLAS 165  
 |||||  
 DB 830 EEEARLAS 837  
 XX  
 RESULT 68  
 ABB91916  
 ID ABB91916 standard; Protein; 934 AA.  
 XX  
 AC ABB91916;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 1127.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 KM Arabidopsis thaliana.  
 OS  
 XX  
 PN W0200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 28-AUG-2001; 2001WO-EP09892.  
 XX  
 PR 28-AUG-2001; 2001WO-EP09892.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Tietjen K, Weidler M;  
 XX  
 DR WPI; 2002-269010/31.  
 XX  
 PT Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms -  
 PS Claim 5; SEQ ID NO 1127; 261pp + Sequence Listing; English.

XX  
 CC The invention relates to identifying target proteins  
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising  
 CC aligning and comparing nucleic acid or amino acid sequences from plant  
 CC with nucleic acid or amino acid sequences from non-plant organisms using  
 CC suitable search parameters, where plant sequences having an E-value  
 CC greater by a factor of 3 than the E-value of most similar non-plant  
 CC sequences are selected. The polypeptides or nucleic acids encoding them  
 CC are useful for identifying modulators. The identified modulators are  
 CC useful as herbicides.  
 XX  
 SQ Sequence 934 AA;  
 XX  
 XX  
 Query Match 0.6%; Score 8; DB 23; Length 934;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 939 DKSQVPTI 946  
 |||||  
 DB 98 DKSQVPTI 105  
 XX  
 RESULT 69  
 AAW21721  
 ID AAW21721 standard; Protein; 968 AA.  
 XX  
 AC AAW21721;  
 XX  
 DT 30-SEP-1997 (first entry)  
 XX  
 DE SH2-A.  
 XX  
 KW SH2 binding domain; LexA-FcERI-gamma-CT; reporter yeast; RBL-2H3 cell;  
 KW Fc-epsilon-RI; detection; protein-protein interaction; phosphorylation;  
 KW tyrosine; signal transduction pathway; activated cell-surface receptor;  
 KW post-translationally modified protein; mast cell activation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 8..93  
 FT Misc-difference 764 /label= SH2\_domain  
 FT Misc-difference 764 /note= "encoded by NAA"  
 FT Misc-difference 933 /note= "encoded by NCG"  
 FT  
 PN US5637463-A.  
 XX  
 PD 10-JUN-1997.  
 XX  
 PF 04-MAY-1995; 95US-0434730.  
 XX  
 PR 04-MAY-1995; 95US-0434730.  
 XX  
 PA (HOF ) HOFFMANN LA ROCHE INC.  
 XX  
 PI Dalton S, Kochan JP, Osborne MA;  
 XX  
 DR WPI; 1997-319067/29.  
 XX  
 DR N-PSDB; AAT77764.  
 XX  
 PT Detection of protein-protein interactions - dependent on  
 PT post-translational modification of one of the protein, also new cDNA  
 PT and protein molecules containing SH2 domains  
 XX  
 PS Claim 18; Fig 7; 30pp; English.  
 XX  
 CC The sequences given in AAW21721-22 represent proteins which contain SH2  
 CC domains. These sequences were identified due to their interaction  
 CC with LexA-FcERI-gamma-CT, a reporter yeast strain. The cDNA sequences  
 CC were isolated from a cDNA library prepared from RBL-2H3 cells, a mast  
 CC cell library which expresses Fc-epsilon-RI. These SH2 domain containing

	CC	proteins may be used in the method of the invention for detecting an interaction between a first test protein and a second test protein.
	CC	The method may be used for detecting protein-protein interactions requiring specific post-translational modifications, e.g. the phosphorylation of tyrosine residues, which is a critical step in the signal transduction pathways of activated cell-surface receptors. It may also be used for identifying amino acid residues that are critical for protein-protein interactions to occur and for identifying novel proteins that bind to post-translationally modified proteins. The method may be used for identifying proteins that can post-translationally modify, or be modified by, other proteins and for identifying molecules that inhibit protein-protein interactions. The novel SH2 proteins may be used in screening inhibitors of mast cell activation.
6Q	Sequence	968 AA;
OY	Query Match Best Local Similarity	0.6%; Score 8; DB 18; Length 968; Matches 8; Conservative 100.0%; Pred.No. 2e+02;
DB	Matches	0; Mismatches 0; Indels 0; Gaps 0;
OY	1075 TLPSESL 1082       	
DB	229 TLPSLESL 236	
RESULT 70		
ID	AAM26624	
XX AC	AAM26624 standard; Protein; 976 AA.	
XX AC	AAM26624;	
DT XX	28-JAN-1998 (first entry)	
DE XX	Signalling Inositol polyphosphate 5-phosphatase SIP-110.	
KM XX	SIP-110: signalling inositol polyphosphate 5-phosphatase; human; signal transduction.	
OS XX	Homo sapiens.	
FH FH	Key Location/Qualifiers	
FT FT	Peptide 370..378 /note= "conserved motif of inositol polyphosphate 5-phosphatase family"	
FT FT	Peptide 456..463 /note= "conserved motif of inositol polyphosphate 5-phosphatase family"	
FT FT	Binding-site 699..702 /label= SHC-PTB /note= "phosphotyrosine binding domain of SH2 and collagen containing protein"	
FT FT	Binding-site 806..809 /label= SHC-PTB /note= "phosphotyrosine binding domain of SH2 and collagen containing protein"	
FT FT	Binding-site 893..896 /label= SH3 /note= "proline-rich SH3 binding motif"	
FT FT	Binding-site 908..911 /label= SH3 /note= "proline-rich SH3 binding motif"	
FT FT	Binding-site 921..924 /label= SH3 /note= "proline-rich SH3 binding motif"	
FT FT	Binding-site 926..931 /label= SH3 /note= "proline-rich SH3 binding motif"	
FT FT	Binding-site 966..969 /label= SH3 /note= "proline-rich SH3 binding motif"	
NN XX	W09722690-A2.	

PD	26-JUN-1997.
XX	
Pf	06-DEC-1996; 96WO-US19515.
XX	
PR	04-DEC-1996; 96US-0759397.
PR	08-DEC-1995; 95US-0569578.
PR	14-DEC-1995; 95US-0008607.
PR	28-MAR-1996; 96US-0624190.
XX	
PA	(CHIR ) CHIRON CORP.
XX	
PI	Kavanaugh WM, Pot D, Williams LT;
XX	
DR	WPI: 1997-341681/31.
N-PDB:	AAT90501.
XX	
PT	Signalling inositol polyphosphate 5-phosphatase, SIP 130 and
PT	related DNA - used for treating abnormal cell growth, regulating
PT	mitogenic activity and calcium signalling
XX	
PS	Disclosure: Page 82-86, 114pp; English.
XX	
CC	This polypeptide comprises a signalling inositol polyphosphate
CC	5-phosphatase (SIP), designated SIP-110, also known as GRB2-
CC	associated inositol polyphosphate 5-phosphatase. SIP-110 binds
CC	both SH3 domains on the GRB2 protein, and modulates signalling of
CC	e.g. ras. It is a splice variant of novel SIP-130 (see AAW6623),
CC	lacking the N-terminal region of SIP-130 including an SH2 domain.
CC	SIP-130 polypeptides and polynucleotides can be used in claimed
CC	methods for modulating phosphatidylinositol 3-kinase activity,
CC	method for modulating protein (MAP) kinase activity, the level of
CC	phosphatidylinositol (3,4,5) triphosphate in a cell, allowing
CC	treatment of diseases associated with abnormal cell growth.
XX	
SO	Sequence 976 AA;
Query Match	0.6%; Score 8; DB 18; Length 976;
Best Local Similarity	100.0%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1075 TLPSLESL 1082       Db 14 TLPSESL 21
RESULT 71	
AAWI8327	
ID	AAWI8327 standard; Protein: 976 AA.
XX	
AC	AAWI8327;
XX	
DT	18-AUG-1997 (first entry)
XX	
DE	BRB2 associating polypeptide GASPLase.
XX	
KM	Inositol polyphosphate 5-phosphatase; GASPLase;
KM	phosphatidylinositol 5-phosphatase; GRB2 associating protein;
KM	signal transduction; cell proliferation; atherosclerosis;
KM	inflammation; psoriasis; cancer; restenosis; therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO9719101-A1.
PD	
XX	29-MAY-1997.
PF	
XX	18-OCT-1996; 96WO-US16671.
XX	
PR	17-NOV-1995; 95US-0560005.
XX	
PA	(REGC ) UNIV CALIFORNIA.
PA	(UNIW ) UNIV WASHINGTON.
XX	

Pt	Jefferson AB, Majerus PW, Pot DA, Williams LT;
Xx	
Dn	WPI; 1997-298053/27.
Dn	N-PsDB; AAt68934.
Xx	
Pt	GRR3 associating polypeptide, GAsPase, nucleic acids and vectors -
Pt	for treating proliferative disorders such as cancer and psoriasis,
Pt	and for screening agonists of inositol polyphosphate 5-phosphatase
Pt	activity
Xx	
Pt	
Xx	
Pt	Claim 1; Page 52-57; 107p; English.
Xx	
Pt	A novel GRR3-associated protein (AAW18327), GAsPase, has inositol
Cc	polyphosphate 5-phosphatase and phosphatidylinositol 5-phosphatase
Cc	activities that are important in growth factor-mediated signal
Cc	transduction. Its amino acid sequence was deduced from an
Cc	isolated GAsPase nucleic acid (AAT68934). GAsPase nucleic acids,
Cc	cells that express these nucleic acids, GAsPase proteins and
Cc	antibodies raised against them can be used in screening,
Cc	therapeutic and other applns., e.g. the treatment of proliferative
Cc	diseases. The polypeptides can also be used in methods for
Cc	determining whether a test cpd. is an agonist or antagonist of
Cc	GRR3/GAsPase interaction and in methods for identifying the
Cc	presence of GRR3 in a sample.
Cc	
Sq	Sequence    976 AA;
Oy	
Dn	Query Match                  0.6%; Score 8; DB 18; Length 976; Best Local Similarity      100.0%; Pred. No. 2e+02; Matches    8; Conservative    0; Mismatches    0; Indels    0; Gaps    0;  1075 TLPSLESL 1082                   14 TLPSTLST 21
RESULT 72	
AAW14002	
ID	AAW14002 standard; Protein; 1187 AA.
Xx	
AC	AAW14002;
Xx	
Dn	24-JUN-1997 (first entry)
Xx	
DE	Mouse SH2-containing inositol phosphatase (SHIP).
Xx	
Kw	SH2-containing inositol phosphatase; SHIP;
Kw	inositol polyphosphate 5-phosphatase; IPPSP; src homology domain 2;
Kw	SH2 domain; signal transduction; leukaemia; cancer; papilloma;
Kw	atherosclerosis; HIV; autoimmune disease; bone resorption;
Kw	inflammation, neurodegeneration; wound healing; diagnosis; therapy.
Os	
Mus sp.	
Xx	
Key	
FH	Location/Qualifiers
FT	Domain
FT	/label= SH2
FT	/note= "src homology domain 2"
FT	549..664
FT	/label= 5-Phosphatase_domain
FT	583..590
FT	/label= 5-Phosphatase_motif
FT	659..676
FT	/label= 5-Phosphatase_motif
FT	910..914
FT	/label= PTB
FT	/note= "phosphotyrosine binding domain target"
FT	1013..1018
FT	/label= PTB
FT	/note= "phosphotyrosine binding domain target"
FT	959..1145
FT	/label= Proline-rich_domain
Xx	

PN	M09712039-A2.
PX	
PD	03-APR-1997.
XX	
PF	27-SEP-1996; 96WO-CA00655.
XX	
PR	14-JUN-1996; 96US-066496Z.
PR	27-SEP-1985; 95US-0006063.
PR	30-NOV-1995; 95US-0007788.
PR	09-APR-1996; 96US-0015217.
XX	
PA	(KRRS/) KRYSTAL G.
XX	
PI	KRYstal G;
DR	WPI; 1997-212898/19.
DR	N-PSDB; AAT60300.
XX	
PT	Inositol polyphosphate-5-phosphatase having SH2 domain - useful for treating cancer and other conditions involving abnormal signalling
XX	
PS	Claim 3; Page 34-38; 89pp; English.
CC	
CC	Murine inositol polyphosphate 5-phosphatase having an SH2 domain (SHIP) (AAW14002) is involved in the control of gene expression and differentiation, proliferation, activation and metabolism of cells, CC patric. via the Ras and phospholipid signalling pathways. It associates with Shc (see also AAW14005) in response to multiple cytokines. Recombinant SHIP can be produced in transformed host cells utilising a nucleic acid (AAT60300) obtd. from B6Sutal cells. SHIP can be used to identify substances which affect the binding of the protein to Shc and/or its inositol phosphatase activity and to screen for (anti)agonists useful for treating cancer and other conditions involving abnormal signalling. Human SHIP (AAW14003) has also been identified.
CC	
SQ	Sequence 1187 AA;
OY	Query Match 0.6%; Score 8; DB 18; Length 1187; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB	1075 TLPSLESL 1082         226 TLPSESL 233
RESULT 73	
AAW14003	
ID	AAW14003 standard; Protein; 1187 AA.
AC	AAW14003;
DT	24-JUN-1997 (first entry)
XX	
DE	Human SH2-containing inositol phosphatase (SHIP).
XX	
KM	SH2-containing inositol phosphatase; SHIP;
KM	inositol polyphosphate 5-phosphatase; TRPSP; src homology domain 2;
KM	SH2 domain; signal transduction; leukaemia; cancer; papilloma;
KM	atherosclerosis; HIV; autoimmune disease; bone resorption;
XX	inflammation, neurodegeneration; wound healing; diagnosis; therapy.
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	Domain 5..102
FT	/label= SH2
FT	/note= "src homology domain 2"
FT	Domain 549..630
FT	/label= 5-Phosphatase_domain
FT	Region 582..589
FT	/label= 5-Phosphatase_motif

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FT Region 658..677
FT /label= 5-Phosphatase_motif
FT Region 909..913
FT /label= PTB
FT /note= "phosphotyrosine binding domain target"
FT 1016..1020
FT /label= PTB
FT /note= "phosphotyrosine binding domain target"
FT 961..1142
FT /label= Proline-rich_domain
XX
XX MO9712039-A2.
XX
XX 03-APR-1997.
XX
XX 27-SEP-1996; 96WO-CA00655.
XX
XX 14-JUN-1996; 96US-0664962.
XX 27-SEP-1995; 95US-0006063.
XX 30-NOV-1995; 95US-0007788.
XX 09-APR-1996; 96US-0015217.
XX
XX (KRYG/) KRYSTAL G.
XX
XX KRYSTAL G.
XX
XX WPI; 1997-212898/19.
XX N-PSDB; AAT60301.
XX
XX Inositol polyphosphate-5-phosphatase having SH2 domain - useful for
XX treating cancer and other conditions involving abnormal signalling
XX
XX Claim 6; Page 49-54; 89pp; English.
XX
XX Human inositol polyphosphate 5-phosphatase having an SH2 domain
XX (SHIP) (AAW14003) is involved in the control of gene expression and
XX differentiation, proliferation, activation and metabolism of cells,
XX partic. via the Ras and phospholipid signalling pathways. It
XX associates with Shc (see also AAW14005) in response to multiple
XX cytokines. Recombinant SHIP can be produced in transformed host
XX cells utilizing a nucleic acid (AAT60301) obtd. from a MO78/MO7-ER
XX cDNA library. SHIP can be used to identify substances which affect
XX the binding of the protein to Shc and/or its inositol phosphatase
XX activity and to screen for (ant)agonists useful for treating cancer
XX and other conditions involving abnormal signalling.
XX
XX Sequence 1187 AA;
XX
XX Query Match 0.64; Score 8; DB 18; Length 1187;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1075 TLPSLESL 1082
XX |||||
XX Db 225 TLPSLESL 232
XX
XX RESULT 74
XX ID AAW26623 standard; Protein; 1189 AA.
XX AC AAW26623;
XX XX
XX XX 28-JAN-1998 (first entry)
XX
XX XX Signalling inositol polyphosphate 5-phosphatase SIP-130.
XX
XX XX SIP-130; signalling inositol polyphosphate 5-phosphatase; human;
XX signal transduction; phosphatidylinositol 3'-kinase;
XX mitogen activated protein kinase; MAP kinase;
XX phosphatidylinositol (3,4,5) triphosphatase; calcium signalling;
XX mitogen; cell growth; cell proliferation; apoptosis; gene delivery;
XX gene therapy.
XX

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XX XX Homo sapiens.
XX OS
XX Key
XX PH Domain
XX FT 5..103
XX FT /label= SH2
XX FT 583..591
XX FT /note= "conserved motif of inositol polyphosphate
XX FT 5-phosphatase family"
XX FT 669..676
XX FT /note= "conserved motif of inositol polyphosphate
XX FT 5-phosphatase family"
XX
XX Binding-site 912..915
XX FT /label= SHC-PTB
XX FT 110..1022
XX FT /label= SHC-PTB
XX FT 1106..1109
XX FT /label= SH3
XX FT /note= "proline-rich SH3 binding motif"
XX FT 1121..1124
XX FT /label= SH3
XX FT /note= "proline-rich SH3 binding motif"
XX FT 1134..1137
XX FT /label= SH3
XX FT /note= "proline-rich SH3 binding motif"
XX FT 1139..1144
XX FT /label= SH3
XX FT /note= "proline-rich SH3 binding motif"
XX FT 1179..1182
XX FT /label= SH3
XX FT /note= "proline-rich SH3 binding motif"
XX FT 186..200
XX FT /note= "isolated peptide"
XX FT 265..278
XX FT /note= "isolated peptide"
XX FT 357..365
XX FT /note= "isolated peptide"
XX FT 434..443
XX FT /note= "isolated peptide"
XX FT 570..579
XX FT /note= "isolated peptide"
XX FT 789..807
XX FT /note= "isolated peptide"
XX FT 701..721
XX FT /note= "isolated peptide"
XX FT 746..760
XX FT /note= "isolated peptide"
XX
XX MO9722690-A2.
XX
XX 26-JUN-1997.
XX
XX PF 06-DEC-1996; 96WO-US19515.
XX
XX PR 04-DEC-1996; 96US-0759397.
XX PR 08-DEC-1995; 95US-0569578.
XX PR 14-DEC-1995; 95US-0008607.
XX PR 28-MAR-1996; 96US-0624190.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Kavanaugh WM, Pot D, Williams LT;
XX WPI; 1997-341681/31.
XX N-PSDB; AAT90500.
XX
XX Signalling inositol polyphosphate 5-phosphatase, SIP 130 and
XX related DNA - used for treating abnormal cell growth, regulating
XX mitogenic activity and calcium signalling
XX
XX Claim 1; Page 87-91; 114pp; English.
XX
XX This polypeptide comprises a novel signalling inositol polyphosphate
XX

```

CC 5-phosphatase (SIP), designated SIP-130, that is capable of binding  
 CC to a phosphotyrosine binding domain (PPTB) of SH2 and collagen  
 CC containing protein (SHC), and which has 5' phosphatase activity for  
 CC a 3' phosphorylated substrate. Its sequence was deduced from a  
 CC human lung cDNA clone (see AAT90500). SIP-110 (see AAW26624) and SIP-N  
 CC (see AAW26625) were identified as splice variants of SIP-130.  
 CC polypeptides can be expressed in transformed host cells. SIP-130,  
 CC active SIP-130 peptides, antibodies and SIP-130-modulating  
 CC polynucleotides can be used in claimed methods for modulating  
 CC phosphatidylinositol 3-kinase activity, mitogen-activated protein  
 CC (MAP) kinase activity, the level of phosphatidylinositol (3,4,5)  
 CC triphosphate in a cell, as well mitogenic activity, allowing  
 CC treatment of diseases associated with abnormal cell growth.

CC Sequence 1189 AA;

Query Match 0.6%; Score 8; DB 18; Length 1189;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1075 TLPSLESL 1082  
 |||||  
 Db 227 TLPSLESL 234

# RESULT 75

AAAY85657  
 ID AAY85657 standard; Protein; 1341 AA.

AC AAY85657;

DT 12-FEB-2001 (first entry)

DE Human Acinus L protein sequence.

KW Chromatin aggregation induction; human; Acinus; AIDS; herpes; diabetes;  
 KW Alzheimer's disease; Parkinson's disease; cardiac infarction;  
 KW brain infarction; adenovirus infection; viral hepatitis.

OS Homo sapiens.

PN WO200061743-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-JP02254.

PR 09-APR-1999; 99JP-0103317.

PA (SHIO) SHIONOGI & CO LTD.

PI Sahara S, Eguchi Y, Tsujimoto Y;

DR WPI; 2000-665130/64.

DR N-PSDB; AAC61196.

PT A novel polypeptide which induces chromatin aggregation but is not  
 PT involved in DNA fragmentation used for the regulation of apoptosis and  
 PT screening of potential apoptosis inhibitors  
 PS Disclosure; Page 60-67; 99pp; Japanese.

CC This invention relates to a polypeptide which induces chromatin  
 CC aggregation. The polypeptide is a fragment of the human Acinus protein.  
 CC Included in the invention is a nucleotide sequence encoding the  
 CC polypeptide, antisense oligonucleotides, antibodies recognising the  
 CC polypeptide sequence, and apoptosis regulating agents containing the  
 CC polypeptide, nucleotide sequence, and sense or antisense  
 CC oligonucleotides. Also included in the invention is a method for  
 CC screening compounds for their activity as chromatin aggregation  
 CC inhibitors, regulators or promoters. The polypeptide induces chromatin  
 CC aggregation within the cell nucleus without inducing DNA fragmentation.  
 CC The polypeptide can be used in the investigation and treatment of

CC diseases in which apoptosis is implicated, including AIDS, Alzheimer's  
 CC disease, Parkinson's disease, cardiac or brain infarction, herpes or  
 CC adenovirus infection, diabetes and viral hepatitis. The present sequence  
 CC represents the human Acinus protein.

CC Sequence 1341 AA;

Query Match 0.6%; Score 8; DB 21; Length 1341;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 EEEBOKER 46  
 |||||  
 Db 1256 EEEBOKER 1263

Search completed: December 18, 2003, 09:13:37  
 Job time : 67 secs

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